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Release 3.0.5AA John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1997 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

on: abular output not generated. Mon May 4 11:44:01 1998; MasPar time 1199.91 Seconds 1331.888 Million cell updates/sec

Description:
Perfect Score:
N.A. Sequence:
Comp: >Q06583 (1-1045) from n-geneseq.seq 1045

1 attccggcttctatggagca......ctggacacagcatgaataaa 1045 taaggccgaagatacctcgt.....gacctgtgtcgtacttattt

Scoring table: TABLE default Gap 6

Nmatch

STD:

Dbase 0; Query 0

Searched: 436399 seqs, 764661465 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

1:em_in 2:em_or 3:em_om 4:em_ov 5:em_pl 6:em_htg 7:em_hum1 8:em_hum2 9:em_ba 10:em_ro 11:em_un 12:em_vi 13:em_pat

genbank105

Database:

14:gb_ro 15:gb_om 16:gb_ov 17:gb_in 18:gb_pl 19:gb_ba 20:gb_st 21:gb_vi 22:gb_ph 23:gb_sy 24:gb_un 25:gb_pat 26:gb_htg 27:gb_pr1 28:gb_pr2

atistics: Mean 10.964; Variance 5.911; scale 1.855

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Match Length DB	BB	ID	Description •	Pred. No.
ш	1045	100.0	1047	15	BOVMET	Bovine metalloproteina	0.00e+00
2	599	57.3	1035	27	HUMMET	Human metalloproteinas	0.00e+00
ω	599	57.3	1062	28	S48568 ·	tissue inhibitor of me	0.00e+00
4	599	57.3	. 1062	27	HUMTIMP2	Human metalloproteinas	0.00e+00
ហ	579	55.4	1007	14	S82718	TIMP-2-testicular tiss	0.00e+00
o	579	55.4	1009	14	S72594	TIMP-2-tissue inhibito	0.00e+00
7	. 577	55.2	969	14	RNU14526	Rattus norvegicus tiss	0.00e+00
œ	575	55.0	1695	14	MUSTIMP2A	Mouse tissue inhibitor	0.00e+00
9	575	55.0	1714	14	MMT IMP 2	M.musculus TIMP-2 mRNA	0.00e+00
10	570	54.5	958	14	RATTIMP	Rattus norvegicus matr	0.00e+00
11	527	50.4	676	14	MUSTIMP2B	M.musculus metalloprot	0.00e+00
12	482	46.1	597	14	CGRNAMP	C. longicaudatus mRNA	0.00e+00
13	452	43.3	555	27	HSTIMP2M	H.sapiens mRNA for tis	0.00e+00
14	ر 2	33.6	814	16	AF004664	Gallus gallus tissue i	1.22e-240

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sequence 2 irom Fatent Sequence 3 from Patent Human collagenase inhi Human fibroblast colla cDNA encoding human me	Human classue inhibitor Gallus gallus metallop Rattus norvegicus tiss Mouse metalloproteinas Mouse tissue inhibitor M.musculus (Balb/C) TI Sequence 14 from patent Rabbit hyperoxia induc Papio cynocephalus (classics)	Human tissue inhibitor Sequence 1 from patent Human tissue inhibitor Sequence 14 from paten Homo sapiens metallopr H. sapiens TIMP3 mRNA f Human tissue inhibitor TIMP-3-tissue inhibitor TIMP-3-tissue inhibitor Human tissue inhibitor Human tissue inhibitor	Human tissue inhibitor
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ALIGNMENTS

RESULT 1	BOVMET	1047 hp	mRNA	MAM	15-550-1990
DEFINITION	Bovine meta	lloproteinas	metalloproteinase inhibitor mRNA, complete cds	complete	cds.
KEYWORDS SOURCE	metalloprot Bovine aort	grosstr metalloproteinase inhibitor. Bovine aorta endothelium, cI	metalloproteinase inhibitor. Bovine aorta endothelium, cDNA to mRNA.		
ORGANISM	Bos taurus Eukaryotae; Vertebrata:	mitochondri Eutheria: /	Bos taurus Bukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Butheria; Artiodactyla; Ruminantia; Pecora;	Ω	hordata; Pecora; Bovoidea;
	Bovidae; Bovinae; Bos.	vinae; Bos.	HI CIOUACCYIA; Numii		cora, boyordea,
AUTHORS	<pre>1 (bases 1 Boone, T.C.,</pre>	(bases 1 to 1047) one,T.C., Johnson,M.;	1 (bases 1 to 1047) Boone, T.C., Johnson, M.J., De Clerck, Y.A. and Langley, K.E.	and Langl	ey,K.E.
TITLE	cDNA clonin related to	g and expres	CDNA cloning and expression of a metalloprote tnase inhibitor related to tissue inhibitor of metalloproteinases	proteinases Steinases	inhibitor
JOURNAL	Proc. Natl.	Acad. Sci.	Proc. Natl. Acad. Sci. U.S.A. 87, 2800-2804 (1990)	304 (1990)	
MEDLINE	90207285		•		
COMMENT	K.E.Langley	and compute, 23-FEB-19	Drait entry and computer-readable sequence [1] kindly submitted by K.E.Langley, 23-FEB-1990, for release after publication.	er public	ation.
FEATURES	٤,	Location/Qualifiers	ifiers		
source	. 1-	11047	•		
	29	/organism="Bos taurus" /db_xref="taxon:9913"	s taurus" on:9913"		
CDS	29 /n	291953 /note="metallo	291953 /note="metalloproteinase inhibitor precursor"	or precui	sor"
	<u>`</u>	/codon_start=1 /db_xref="PID:q163342"	1 :q163342"	1	
	II.	ranslation=	/translation="MGAAARSLPLAFCLLLLGTLLPRADACSCSPVHPQQAFCNADIV TRAKAVNKKEVDSGNDIYGNDIKRIOYEIKOIKMFKGPDODIEFIYTAPAAAVCGVSL	TLLPRADAC	SCSPVHPQQAFCNADIV
	MI	GGKKEYLIAGK!	DIGGKKEYLIAGKAEGNGNMHITLCDFIVPWDTLSATQKKSLNHRYQMGCECKITRCP MIPCYISSPDECLMMDWVTEKNINGHQAKFFACIKRSDGSCAWTRGAAPPKQEFLDIE	TISATOKKS CIKRSDGSC	SLNHRYQMGCECKITRCP SAWYRGAAPPKQEFLDIE
sig_peptide		291368			
mat_peptide	>	/note="metalloproteinase 369950		inhibitor signal	peptide"
polyA_signal	_	/note="metall: 10421047	<pre>/note="metalloproteinase inhibitor" 1042 1047</pre>	or"	

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          CAGGACTCCTGGGGCCAATTGACAGTGTCCAAGAGTTCAGACTGGTCCAGCTCCGACATC
                                                  CGCGGAGCACCCCCCAAGCAGGAGTTTCTGGACATCGAGGACCCGTAAGCAGGCCAC
                                                                                     ggacaccaggccaagttcttcgcctgcatcaagagaagcgacggctcctgcgcctggtac
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Boone, T.C., Johnson, M.J., De Clerck, Y.A. and Langley, K.
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Human fetal aorta, cDNA to mRNA.
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IRAKAVSEKEYDSGNDIYGNPIKRIQYEIKQIXMFKGFEKDIEFIYTARSSAVCGVSL
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MIPCYISSPDECLMMDWYTEKNINGHQAKFFACIKRSDGSCAWYRGAAPPKQEFLDIE
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/product="tissue inhibitor of metalloproteinase
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IRAKAYSEKEVDSGNDIYGNPIKRIQYEIKQIKMEKGPEKDIEFIYTAPSSAVCGVSL
DVGGKKEYLLAKRAEGGGKMHITLCDBIVFMPDTLSTTQKKSLAHRRYQMCCECKLTIRCP
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DEFINITION

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                                               CCCCCTCCTCGGCAGTGTGTGGGGGTCTCGCTGGACGTTGGAGGAAAGAAGGAATATCTCA
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Tissue inhibitor of metalloproteinases-2 (TIMP-2) mRNA expression in tumor cell lines and human tumor tissues
J. Biol. Chem. 265 (23), 13933-13938 (1990)
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kindly submitted by W.G.Stetler-Stevenson,
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Human melanoma cell
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ilarity 89.6%;
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/gene="TIMP"
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/db_xref="FID:G339707"
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DVGGKKEYLIAGKAEGDGKMHITLCDFIVPMDTLSTTQKKSLNHRYQMGCECKITRCP
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/db_xref="taxon:9606"
/map="Xpl1.3-pl1.23"
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Purification, CDNA cloning, and developmental changes in steady-state mRNA, level of rat testicular tissue inhibito metalloproteases-2 (TIMP-2)
J. Androl. 17 (3), 263-275 (1996)
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                                                                                                                                                                                                                                                               entry [NCBI gibbsq 179018] from Fig.
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                  /product="TIMF-2"
/db_xref="FID:91881814"
/db_xref="FID:91881814"
/translation="MGAARSLRLAEGLLLATLLRPADACSCSPVHPQQAFCNADVV
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DVGGKKEYLLAGKAEGDGKMHITLCDEIVPRDTLSIYQKKSLMHRYQMGCECKITRCP
MIPCYISSPDECLWMDWVTEKSINGHQAKFFACIKRSDGSCAWYRGAAPPKQEFLDIE
DP"
                                                                                                                 This sequence comes
                                                                                                                                                           /gene="TIMP-2"
219. .881
                                                                                                /codon_start=1
                                                                                                              /note="testicular tissue inhibitor of This sequence comes from Fig. 2A"
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                  ccacccagaagaagagcctgaaccacaggtaccagatgggctgtgagtgcaagatcactc
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Santoro,M., Battaglia,C., Zhang,L., Carlomagno,F., Martelli,M.L.,
Salvatore,D. and Fusco,A.
Cloning of the rat tissue inhibitor of metalloproteinases type 2
(TIMP-2) gene: analysis of its expression in normal and transformed thyroid cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 15344]] from the original journal article.
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/translation="MGAAARSLRLALGLLLLATLLRPADACSCSPVHPQQAFCNADVV
/translation="MGAAARSLRLALGLLLLATLLRPADACSCSPVHPQQAFCNADVV
IRAKAVSEKEVDSGNDIYGNPIKRIQXEIKQIKMFKGPDKDIEFIYTAPSSAVCGVSL
DVGGKKEYLLAGRAEGDGKMHITLCDFIVFMDYLSITQKKSLNHRYQMGCECKITRCP
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1 (bases 1 to 969)
Cook, T.F., Burke, J.S.,
                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (08-SEP-1994) N.C. Partridge, School of Medicine, Department of Pharm.
South Grand, St. Louis, MO 63104, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cloning and regulation of rat tissue inhibitor of metalloproteinases-2 in osteoblastic cells Arch. Biochem. Biophys. 311 (2), 313-320 (1994)
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Partridge, N.C.
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                                                                                                                                                                                                                                                                                   /clone="pRT4"
/clone_11b-"UMR 106-01 library of N.C. Partridge"
/cell_line="UMR 106-01 rat osteosarcoma"
/cell_type="osteoblast"
                                                                                                                                                                                                                                                                                                                                        /strain="Sprague-Dawley"
/db_xref="taxon:10116"
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Score 577; DB 14;
Pred. No. 0.00e+00;
0; Mismatches 91;
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       1 (bases 1 to 1695)
Shimizu,S., Malik,K.,
Koiwai,O.
                                     Eukaryotae; mitochondrial eukaryotes; Metazoa;
Vertebrata; Eutheria; Rodentia; Sciurognathi; I
Murinae; Mus.
                                                                               extracellular protein; matrix metalloproteinase inhibitor of metalloproteinase. Mus musculus (strain BALB/c, sub_species domestilambda gtil) embryo cDNA to mRNA.
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larity 87.9%;
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DVGGKKEYLIAGKAEGDGKMHITLCDFIVPWDTLSITQKKSLNHRYQMGCECKITRCP
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/product="tissue inhibitor of metalloproteinases"
/db_xref="pib:9202052"
/translation="MGAAARSLRLALGLLLLASLVRPADACSCSPVHPQQAFCNADVV
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/dev_stage="embryo"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (14-OCT-1991)
Cancer Center Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shimizu,S.,
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                                                                    /gene="mouse TIMP-2"
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/gene="mouse TIMP-2"
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DVGGKKEYLIAGKAEGDGKMHITLCDFIVPWDTLSITQKKSLNHRYQMGCECKITRCP
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                                                       /product="mature Tissue
                                                                                                                                                                                                               /db_xref="PID:g54802"
/db_xref="SWISS-PROT:P25785"
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/clone_lib="gtll"
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Institute, 1-1 Kanokoden, Chikusa-ku,
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  Rattus norvegicus (tissue library: lambda gt10) female me to mRNA. Rattus norvegicus (tissue library: lambda gt10) female me to mRNA. Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha;
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                                                                                                                                                                                                                                                            GGAATGACATCTATGGCAACCCCCATCAAGAAGGATTCAATATGAGATCAAGCAGATAAAGA 440
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                                                                                                                                                                                                                                                                                                                           TTTGCAATGCAGACGTAGTGATCAGGGCCAAAGCAGTGAGCGAGAAGGAGGTGGATTCCG
                                                                                                          gtggggtctcgctggacattggaggaaagaaggagtatctcattgcagggaaggccgagg
                                                                                                                           GCGGGGTCTCGCCTGGACGTTGGAGGAAAAGGAAGGAATATCTAATTGCAGGGAAGGCGGAAG
                                                                                                                                                                           tgttcaagggacctgatcaggacatagagtttatctacacagcccccgccgctgccgtgt
                                                                                                                                                                                                                                          gcaacgacatctacggcaaccccatcaagcggattcagtatgagatcaagcagataaaga
                                             ggaatggcaatatgcatatcaccctctgtgacttcatcgtgccctgggacaccctgagtg
                                                                                                                                                                                                               TGTTCAAAGGACCTGACAAGGACATCGAATTTATCTACACGGCCCCCTCCTCAGCAGTGT
                                                                                                                                                                                                                                                                                                                                                                           ggacgctgctcccccgggccgacgcctgcagctgctccccggtgcacccgcaacaggcgt 400
                                                                                                                                                                                                                                                                                                                                                                                                                                          cgcccgccatgggcgccgccgccgcagcctgccgctcgcgttctgcctcctgctgctgg 340
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Gibbons,K.L., O'Grady,R.L. and Piper,A.A.
Rat tissue inhibitor of metalloproteinases-2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 54.5%;
Similarity 88.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               מ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /function="tissue inhibitor of matrix metallo
(type 2)"
/product="matrix metalloproteinase inhibitor"
869. .958
a 297 c 288 g 169 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="matrix metalloproteinase inhibitor"
/db_xref="pID:g1141730"
/db_xref="pID:g1141730"
/translation="McAARSILHALGILLLATILRPADACSCSPVHPOQAFCNADVV
IRAKAVSEKEVDSGNDIYGNPIKRIQYEIKQIKMFKGGDKDIEFIYNAPSSANCGVSL
DVGGKKEYLIAGKAEGDGKMHITLCDFIVPMDTLSITQKKSLNHRYQMGCECKITRCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene=
209. .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="mammary"
/tissue_lib="lambda gt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_type-"carcinoma"
/sex-"female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref-"taxon:10116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Rattus norvegicus"
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                                                                                                                                                                                            TIMP-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 570; DB 14;
Pred. No. 0.00e+00;
0; Mismatches 87
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Matches 60
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CCGCCATGGGCGCCGCGCCAGCCTCCGGCTGCCGCCACGGCCTCCTGCTAGCCT 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Differential regulation of TIMP-1 and TIMP-2 mRNA expression normal and Ha-ras-transformed murine fibroblasts
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Vertebrata; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M.musculus metalloproteinase inhibitor (TIMP-2)
M93954
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     metalloproteinase inhibitor.
Mus musculus (strain C3H) cDNA to
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                                                                  50.4%;
Similarity 89.2%;
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co,K.J., Hayden,L.J., Sharma,R.R.,
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                                                                                                                            162
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                                                      Conservative
                                                                                                                                                                                                                                                                                                                    /strain="C3H"
/db_xref="taxon:10090"
/cell_line="C3H 10T1/2"
/cell_type="fibroblasts"
9. .671
                                                                                                                                                           /evidence-experimental
/product="TIMP-2"
/product="TIMP-2"
/db_xref="PID:9202054"
/translation="MGAARSIRLAHGLLLLASILRPADACSCSPVHPQQAFCNADVV
/translation="MGAARSIRLAHGLLLLASILRPADACSCSPVHPQQAFCNADVV
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DVGGKKEYLIAGKAEGGGKMHITLCDEIVPWDTLSITQKKSLNHRYQMGCECKITRCP
                                                                                                                                                    MIPCYISSPDECLWMDWVTEKSINGHQAKFFACIERSDGSCAWYRGAAPPKQEFLDIE
                                                                                                                                                                                                                                               function="metalloproteinase
                                                                                                                                                                                                                                                               codon_start=1
                                                                                                                                                                                                                                                                             /gene="TIMP2"
                                                                                                                                                                                                                                                                                            /gene="TIMP2"
). :671
                                                                                                                                                                                                                                                                                                                                                                                        organism="Mus musculus"
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Pred. No. 0.00e+00;
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha;
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X75924
                                                                                                                                                                                                                                                              g414876
                                                                                                                                                           Suzuki,Y.
                                                                                                                                                                                                                                      long-tailed hamster
                                                                                                                                                                                                                                                 Tissue inhibitor of metaro
                                                                                    Submitted (02-NOV-1993) Y. Suzuki, 370-05 Akaiwa 2716, Chiyoda-machi,
                                                                                                           Direct Submission
                                                                                                                                              Unpublished
                                                                                                                                                                                    Cricetinae;
                                                                                                                                                                        (bases 1 to
                                                                                                                                                                                                                                                                                      longicaudatus mRNA
                                                                                                                                   (bases 1 to 597)
          /organism="Cricetulus longicaudatus"
/db_xref="taxon:10030"
/clone_lib="chinese hamster ovary"
/clone="K1"
                                                                      Location/Qualifiers
/cell_type="ovary"
                                                                                                                                                                        Eutheria; Rodentia; Cricetulus. to 597)
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                                                                                   Suntory Pharm-Tech Center,
Ohra-gun, Gumma, JAPAN
                                                                                                                                                                                               Myomorpha;
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                                                                                                                                                                                                                        ggagcagcacccccaagcaggagtttctggacatcgaggaccc 947
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                                                                                                                                                                                                                                                                                              CACCAGGCCAAGTTCTTTGCCTGCATCAAGAGAAGTGACGGCTCTTGCGCATGGTACCGC
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                                                                                                                                                                                                                                                                                                                                                                                                CACAGGTACCAGATGGGCTGCGAGTGCAAGATCACACGCTGCCCCATGATCCCATGCTAC
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1 (bases 1 to 555)
Malik,K.T.A.
Direct Submission
                                                                     human.
Homo sapiens
                                                     Eukaryotae;
                                           Vertebrata;
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larity 91.3%;
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/db_xref="pin:9414877"
/db_xref="pin:9414877"
/translation="RACSCSPVHPQQAPCNADVVIRAKAVSEKEVDSGNDIYGNPIKR
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IQYEIKQIKMFKGPDKDLEFIYTAPSSAVCGVSLDVGGKKEYLIAGKABGDGKMHITL
CDFIVPHDTLSTTQKKSLNHRYQMGCECKITRCPMIPCYISSPDECLMMDWVTEKSIN
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                                        mitochondrial eukaryotes; Metazoa; Chordata; Eutheria; Primates; Catarrhini; Hominidae; H
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                       TTCTTCGCCTGCATCAAGAGAAGTGACGGCTCCTGTGCGTGGTACCGCGGCGCGGCGCCCC
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                                                               GACGAGTGCCTCTGGATGGACTGGGTCACAGAGAAGAACATCAACGGGCACCAGGCCAAG
                                                                                                                      ATGGGCTGCGAGTGCAAGATCACGCGCTGCCCCATGATCCCGTGCTACATCTCCTCCCCG
        ttcttcgcctgcatcaagagaagcgacggctcctgcgcctggtaccgcggagcagcaccc
                                                                                                                                                                             atcgtgccctgggacaccctgagtgccacccagaagaagagcctgaaccacaggtaccag
                                                                                                                                                                                                        ATCGTGCCCTGGGACACCCTGAGCACCACCCAGAAGAAGAGCCTGAACCACAGGTACCAG
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Similarity 90.8%;
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Conservative

Length Indels 555; 0

Gaps

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420 735

795

855 480 300 615

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Chemical Industries, 530 Chokeiji, Takaoka City, Toyama 933, Japan
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Malik,K., Sejima,H., Aoki,T. and Iwata,K.
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                                                                                                                                                                              /gene="TIMP-2"
547. .555
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/product="Tissue inhibitor of metalloproteinases,
/db_xref="pin:937181"
/db_xref="SWISS-PROT:P16035"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="GIN-1"
                                                                                                               /note="cloning primer-derived (3')"
148 c 159 g 101 t
                                                                                                                                                                                                                                                                                           /translation-"SPVHPQQAFCNADVVIRAKAVSEKEVDSGNDIYGNPIKRIQYEI
KQIKMFKGPEKDIEFIYTAPSSVVCGVSLDVGGKKEYLIAGKAEGDGKMHITLCDFIV
                                                                                                                                                         /gene="TIMP-2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="TIMP-2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="human fibroblast'
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Score 452; DB 27;
Pred. No. 0.00e+00;
0; Mismatches 51
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     ctacggcaaccccatcaagcggattcagtatgagatcaagcagataaagatgttcaaggg
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Eukaryotae; Archosauria; Aves; Neognathae; Galliformes;
Vertebrata; Archosauria; Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (17-MAY-1997) University of California - San Diego, Department of Chemistry and Biochemistry, 9500 Gilman Drive, Jolla, CA 92093-0654, USA
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Aimes, R.T., Li, L., Weaver, B.,
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                                                                                                                                                                                                                                                                                             /product="tissue inhibitor of metalloproteinase-2"
254 c 259 g 125 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   precursor"
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; H
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/tissue_type="placenta"
join(044381:2218. .2691,U44382:1.
U44384:1. .539,1. .853)
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                                                                         /organism="Homo sapiens"
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/product="fissue inhibitor of metalloproteinases-2"
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AKAVSEKEVDSGNDIYGNPIKRIQYEIKQIKMFKGPEKDIEFIYTAPSSAVCGVSLDV
GGKKEYLIAGKAEGDGKMHITLCDFIVPMDTLSTTQKKSLNHRYQMGCECKITRCPMI
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Post-processing:

Minimum Match 0% Listing first 45 summaries

Database:

n-geneseq30
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33

"tatistics: Mean 9.000; Variance 5.747; scale 1.566

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES :

Result	Score	Query Match	Query Match Length	DB.	ID	Description	Pred. No.
1	1045	100.0	- :	- }	Q06583	Sequence encoding bov	0.00e+00
2	1045	100.0	1045	13	Q73087	Bovine metalloprotein	0.00e+00
w	599	57.3		μ.	Q06584	Sequence encoding hum	0.00e+00
•	597	57.1		13	Q73088	Human metalloproteina	0.00e+00
₅	529	50.6			Q05940	Complete sequence of	0.00e+00
σ	502	48.0		ш	Q05938	TIMP-2 metalloprotein	0.00e+00
7	476	45.6		28	T64341	Human small tissue in	2.90e-291
œ	474	45.4		~	Q05939	TIMP-2 metalloprotein	6.30e-290
9	188	18.0		21	T26262	Human gene signature	1.21e-100
10	83	7.9	675	22	T34433	Tissue inhibitor of m	7.52e-34
. 11	83	7.9	675	32	T80986	Tissue inhibitor of m	7.52e-34
c 12	78	7.5	1047	N	Q10572	Human Natriuretic Pep	8.44e-31
13	72	6.9	1047	N	Q10572	Human Natriuretic Pep	3.60e-27
14	60	5.7	820	16	T02361	TIMP-3 clone Timp3HCM	4.93e-20
15	60	5.7	963	16	T02360	TIMP-3 DNA clone Timp	4.93e-20
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16 60 5.7 1240 16 T02359 TIMP-3 DNA clone Timp 4.93e-20 1776 160 5.7 1276 14 Q82747 Human tissue inhibito 4.93e-20 18 60 5.7 1285 15 Q86744 TIMP-3 metalloprotein 4.93e-20 51 4.9 51 13 Q73095 Human metalloproteina 7.99e-15 51 4.9 51 13 Q73095 Human metalloproteina 7.99e-15 51 4.9 51 13 Q73093 Human metalloproteina 7.99e-15 51 4.9 51 14 Q82741 Chicken tissue inhibit 0.401e-13 7.99e-15 7.99e-1	00000		o o	იი	0000
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ALIGNMENTS

Query Match 100.0%; Best Local Similarity 100.0%; Matches 1045; Conservative

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Claim 12; Fig 1; 65pp; English.
073087 encodes R62768 bovine metalloproteinase inhibitor (MI), it may be used to inhibit tumour cell dissemination and for treating rheumatoid arthritis, dystrophic epidermolysis bullosa; emphysema and osteoporosis. The DNA may be used to detect MI gene disorders. Sequence 1045 BP; 219 A; 350 C; 311 G; 165 T;
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RESULT ID Q

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13-JUL-1995 (first entry)
Human metalloproteinase inhibitor; tumour cell dissem
Metalloproteinase inhibitor; tumour cell dissem
rheumatoid arthritis; dystrophic epidermolysis
amohysema; osteoporosis; MI gene disorders; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                large-scale recombinant inhibitor prodn.

Claim 12; Fig 2; 65pp; English.

It claim 12; Fig 2; 65pp; English.

It claim 12; Fig 2; 65pp; English.

Claim 12; Fig 2; Fig 2; 65pp; English.

Claim 12; Fig 2; Fig 
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(CHIL-) CHICARENS HOSPITAL LOS ANGELES.

(CHIL-) CHICARENS HOSPITAL LOS ANGELES.
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19-MAY-1989; US-355027.
29-MAR-1990; US-501904.
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253..915
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Pred. No. 0.00e+00;
0; Mismatches 78
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olysis bullosa;
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                                                                                                                                                                                                                                                                                                    resulting from matrix metallo-proteinase activity and in diagnosis, detection and purificn.

Suisclosure; Fig 7; 54pp; English.

TIMP-2 was isolated from human melanoma cell-conditioned media and the mino acid sequence determined. A probe was synthesised based upon the protein sequence information. It was used to screen a LambdaGem-4 cDNA library prepared from human melanoma cells. 239 positives were identified from a total of 750,000 plaques screened. Further analysis and screening with additional probes eliminated most of the clones. Clone pSS38 was isolated and the nucleotide sequence of the cDNA insert was determined. The deduced amino acid sequence showed excellent agreement with that derived by directly sequencing the TIMP-2 protein.

See also US7317407 and WO9010228.

See also US7317407 and WO9010228.

See also OS937, R06746-R06750, R06894-R06895 and Q05938-Q05939.
                                                                                                                                                                                    Query Match
Best Local S
Matches 62
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13-MAR-1990; 494796.
21-MAR-1989; US-38334.
17-JUL-1989; US-380431.
18-AUG-1989; US-395453.
13-MAR-1990; US-494796.
(USSH ) NAT INST OF HEALTH.
Stetler-Sevenson WG, Liotta
WPI; 90-290097/38.
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16-JAN-1991 (first entry)
Complete sequence of humam TIMP-2 from clone pSS38.
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21-AUG-1990
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tgtagtgatcagggccaaagcggtcagtgagaaggaagtggactctggaaacgacattta
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llarity 90.1%;
Conservative
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Pred. No. 0.
0; Mismatcl
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.00e+00;

    used to
activity

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131 T;
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                                                                                                                                    /product-part of TIMP-2
US7494796-A.
US7494796-A.
21-AUG-1990: 494796.
21-MAR-1989; US-326334.
17-JUL-1989; US-380431.
18-AUG-1989; US-395453.
18-AUG-1989; US-494796.
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Q05938 stand
Q05938;
Q05938;
16-JAN-1991
                                                                                                                                                                                                                                                                            16-JAN-1991 (first entry)
TIMP-2 metalloproteinase i
matrix metalloproteinase i
                                                                                                                                                                                                                                                                                                                                                                          1009
         New matrix metallo-proteinase inhibitor - used to treat dise
resulting from matrix metallo-proteinase activity and in
diagnosis, detection and purificn..
Disclosure; Fig 6A; 54pp; English.
TIMP-2 was isolated from human melanoma cell-conditioned med
the maino acid sequence determined. A probe was synthesised
based upon the protein sequence information. It was used to
                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                   (USSH ) NAT INST OF HEALTH.
Stetler-Sevenson WG, Liotta
WPI; 90-290097/38.
                                                                                          P-PSDB; R06896
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Matches 60
Homo sapiens.
J09000265-A.
07-JAN-1997.
22-JUN-1995;
22-JUN-1995;
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                                                          Human small tissue inhibitor metalloprotease Human; small tissue inhibitor metalloprotease brain tumour; malignant; diagnosis; ds.
                                                                                               T64341 standard;
T64341;
21-MAY-1997 (fi
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Similarity 89.3%;
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156307. JP-156307

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Q05939 standard; DNA; 832 BF Q05939;
16-JAN-1991 (first entry)
TIMP-2 metalloproteinase inh
matrix metalloproteinase inh
Synthetic.
Key
Location/Qua
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The present sequence is that of the human small tissue inhibitor metalloprotease 2 (TIMP2) DNA. Expression of this sequence is negatively correlated with brain tumour malignancy, i.e. relative expression levels are: normal brain tissue > astrocytoma > anaplastic astrocytoma > glioblastoma. By determining the level of TIMP 2 expression in human brain tissue, the malignancy of cerebral tumours can be evaluated.

Sequence 671 BP; 177 A; 184 C; 196 G; 114 T;
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Claim 1; Page 5; 5pp;
The present sequence i
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WPI; 9
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97-112848/11
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565; Conser
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llarity 89.8%;
Conservative
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                                  inhibitor-encoding
inhibitor; TIMP-2;
                                                                                ВP
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Bisclosure, Fig 6B; 54pp; English.

TIMP-2 was isolated from human melanoma cell-conditioned media and the amino acid sequence determined. A probe was synthesised based upon the protein sequence information. It was used to screen a LambdaGem-4 cDNA library prepared from human melanoma cells. 239 positives were identified from a total of 750,000 plaques screened. Further analysis and screening with additional probes eliminated all but two clones (pSS15 and pSS18). Both were sequenced and found to encode CSC-21K (=TIMP-2), a novel metalloproteinase inhibitor. See also US7317407 and WO9010228.

See also US7317407 and WO9010228.

See also US7317407 and WO9010228.

See also US7317407 and WO9010228.
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Best Local Similarity
Matches 569; Conser
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/product-part of TIMP-2
US7494796-A.
21-AUG-1990: 494796.
13-MAR-1999: US-326334.
17-UL-1989: US-380431.
18-AUG-1989: US-395453.
18-AUG-1989: US-395453.
13-MAR-1990: US-494796.
(USSH ) NAT INST OF HEALTH.
Stetler-Sevenson WG, Liotta L
WPI: 90-290097/38.
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C double-stranded DNA) which comprises one of the 7837 "GS" sequences
C given in T19001-T26837 and which is able to hybridise to part of
C human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
C sequences were obtained from 3'-directed cDNA libraries prepared
C from various human tissues; synthesis of cDNA was initiated from the
C 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
C untranslated sequence is unique to a particular mRNA species, almost
C all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
C is constructed so as to reflect accurately the relative abundance of
C different mRNAs in the particular tissue from which it was derived.
C The appearance frequency of a given GS in a cDNA library can be
C determined (esp. using primers and probes derived from the GS
C sequences) as a means of diagnosing abnormal cell function or for
C recognising different cell types.
S Sequence 302 BP; 75 A; 96 C; 75 G; 53 T;
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Best Local :
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 TIT 10
T34433 standard;
T34433;
09-OCT-1996 (fir
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Matsubara K, Okubo K;
MPI; 95-206931/27.

Identifying gene signatures in 3'-directed human cDNA library
for diagnosis of abnormal cell function, by preparing cDNA the
for diagnosis of abnormal cell function, by preparing cDNA the
for diagnosis of abnormal cell function, by preparing cDNA the
for diagnosis of abnormal cell function, by preparing cDNA the
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
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WO9514772-A1.
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(OKUB/) OKUBO K.
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Similarity 87.5%;
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20-JUN-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A full-length cDNA clone (T34433) codes for human tissue inhibitor of metalloproteinase-4 (TIMP-4) (R98265), which was identified as a novel member of the TIMP family. The cDNA clone was obtd. from a cDNA library derived from an early stage human brain. It can be used for prodn. of recombinant TIMP-4, using e.g. Escherichia coll, COS or insect cell hosts. It can also be used in gene therapy, or to design probes for use in diagnosis of a disease, or a susceptibility to a disease, related to a mutation in the human TIMP-4 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diseases,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME
Greene JM, Rosen CA;
WPI; 96-300644/30.
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Tissue inhibitor of metalloproteinase-4; TIMP-4; cancer;
bone resorption; Paget disease; gene therapy; diagnosis;
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A full-length cDNA clone
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13-DEC-1994; WO-U14498.
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                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PT DNA encoding a tissue inhibitor of metallo:proteinase(s), TIMP-4 - pr for production of recombinant protein for treating tumours, arthritis, etc., and for contraception protein as a signated contraception contraception contraception. Timp-4 contraces and growth, osteoperosis, pulmonary emphysema, periodontal disease and contended arthritis, osteoperosis, pulmonary emphysema, periodontal disease and contended arthritis, and for contraception. Timp-4 contraception contraception contraception contraception contraception contraception contraception. Timp-4 contraception contraception contraception contraception contraception contraception contraception contraception contraception. Timp-4 contraception contraception contraception contraception contraception contraception. Timp-4 contraception contraception contraception contraception contraception contraception contraception contraception. Timp-4 contraception contra
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Tissue inhibitor of metalloproteinase; TIMP-4; Incyte Clone No.
metalloprotease; tumour metastasis; angiogenesis; growth; osteoo
osteoporosis; pulmonary emphysema; periodontal disease; diabeti
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18-JAN-1996; US-588163.
(INCY-) INCYTE PHARM INC.
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US5643752-A.
01-JUL-1997.
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Pred. No. 7.52e-34;
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Natriuretic protein receptor B for diagnosis and treatment of kidney failure, heart failure, hyperaldosteronism, glaucoma etc. Claim 3; Fig 1; 49pp; English.

The sequence was derived from the DNA encoding natriuretic peptide receptor B, NPRB, having guanyl cyclase (GC) activity and protein kinase activity. The DNA can be inserted into expression vectors for the protein, of the protein, opt after being mutated to produce NPRB analogues. The protein has a mol wt. of 115 kD (calculated MrRB analogues. The protein (or variants) can be used in treatment of 114,952).
                                                                                                                                                                                                              (GETH ) GENENTECH INC. Chang M, Goeddel D, Lowe WPI; 91-036711/05.
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Human Natriuretic Peptide Receptor B.
NPRB; ANP; BNP; CNP; kidney failure;
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Modified -site 600..602
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Modified -site 349..351
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Modified -site 277...
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Modified -site 244..246
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Modified -site 195..197
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Modified -site 161..163
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Modified -site 35..3
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Q10572 standard; DNA; 1047
Q10572;
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                                                                                                                                           dnndvykvntngdaymvvsgnngrng
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                                                                                                                                                                                                                                                                                                                       gggccgcgctggtctggacggcactccgcgggcgcgctctcctctccggccctcactcgc
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                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Natriuretic protein receptor B - for diagnosis and treatment of kidney failure, heart failure, hyperaldosteronism, glaucoma etc. Claim 3; Fig 1; 49pp; English.

The sequence was derived from the DNA encoding natriuretic peptide receptor B, NPRB, having guanyl cyclase (GC) activity and protein kinase activity. The DNA can be inserted into expression vectors for the prodn. of the protein, opt. after being mutated to produce
                                                                                                                                                                                                                                                                                                                                                                                       also be prepd
                                                                                                                                                                                                                                                                                                                                                                                                              natriuretic peptide disorders, affinity chromatography. Anti
                                                                                                                                                                                                                                                                                                                                                                                                                                 for the prodn. of the protein, opt. after being mutated to produce NPRB analogues. The protein has a mol wt. of 115 kD (calculated Mr-114,952). The protein (or variants) can be used in treatment of natriuretic peptide disorders, and also to isolate peptides using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chang M, Goeddel D, Lowe WPI; 91-036711/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Natriuretic Peptide Receptor B.
                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hyperaldosteronism; glaucoma; guanyl cyclase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NPRB; ANP; BNP; CNP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; Q10324.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= N-glycos_site
Modified -site 600..602
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Modified -site 161...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "GC and protien kinase activity"
Modified -site 24..26
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23-JUN-1989; US-370673.
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!odified -site 349...
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/odified -site 277...
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Modified -site 35..37
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nes 71; Conse
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hgvtgnvvmdknndrntdnvnwamgdndsgdnnnaahysganknnwwtgrnnnwvkgann
                                                                              nnrarndngvnngnsnmnnnagcnydgnnnyanvnnntnnnggtrndgnrnvnkmngrry 373
                                                                                                                                                            yndvngnsnragntratgrnwndnrtrnnananrnanntvnvntyrnnnnnnnynnnnnrn 313
                                      gcgcccgcggagtgccgtccagaccagcgcggccccggcggagaggggagcgccccgagc
                                                                                                                      gcaccccgcgacctagagccaagaaagtttgtgtgtgggagtgagggccggagagggagagc 177
                                                                                                                                                                                                     gccgcccccagccagctctcgcttccgcgccccccccgcgcccccgcgcc-tcctcgct 117
                                                                                                                                                                                                                                                                                                                                                                          1047 BP;
                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                        87 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ö
                                                                                                                                                                                                                                                                                                                                                                                                              ders, and also to isolate peptides Antibodies with affinity for NPRB
                                                                                                                                                                                                                                                                                       247; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                        15 C;
                                                                                                                                                                                                                                                                                                             72; DB 2; I
No. 3.60e-27;
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                                                                                                                                                                                                                                                                                          509;
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                                                                                                                                                                                                                                                                                                                                Length 1047;
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cell disorders, etc.

Example 4; Page 69-70; 112pp; English.

CDNA clone Timp3HCM-3 (T02361) codes for a natural variant (R84217) of tissue inhibitor metalloproteinase 3 (TIMP-3), lacki a portion of the N-terminus of the mature protein in comparison with the clone Timp3Clone 7 product (R84215). Timp3HCM-3 was isolated from a human colonic mucosa cDNA library using primers
                                                                                                                                                                                                                                                                                                                                                                                   29.FEB-1996 (first entry)
TIMP-3 clone Timp3HCM-3.
TIMP-3; tissue inhibitor metalloproteinase type three; cancer; inflammation; emphysema; embryo implant modulation; arthritis; dystrophic epidermolysis bullosa; peridontal disease; ulcer; scleroderma; vulnerary; gene therapy; ss.
                                                                                                                                                                                                                                               WO9509918-A1.
13-APR-1995.
04-OCT-1994; U11241.
06-OCT-1993; US-134231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T 14
T02361 standard; DNA; 820
                                                                                                                                New tissue inhibitor metallo:proteinase cancer, inflammation, emphysema, embryo
                                                                                                                                                                              P-PSDB; R84217
                                                                                                                                                                                           Koski RA, Silbiger
WPI; 95-155259/20.
                                                                                                                                                                                                                                   (AMGE-)
                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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A, Silbiger SM;
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Best Local S
Matches 16
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Best Local
                                                   prodn. Gence
e.g. of emphysema.
963 BP;
                                                                                          example 4; Page 67-68; 112pp; English.

CDNA clone Timp3clone2 (T02360) codes for a natural variant (R84216) of tissue inhibitor metalloproteinase 3 (TIMP-3), lacking part of the signal peptide of the Timp3clone 7 product (R84215). The cDNA clone was isolated from a human 20 and 24 wk foetal kidney cDNA library using primers based on TIMP sequences. The cDNA is pref. expressed in Escherichia coli for use in recombinant TIMP-3
                                                                                                                                                                                                                                                                                                                                                                                                                TIMP-3; tissue inhibitor metalloproteinase type three; cancer; inflammation; emphysema; embryo implant modulation; arthritis; dystrophic epidermolysis bullosa; peridontal disease; ulcer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                based on TIMP sequences. The cDNA is pref. expressed in Escherichia coli for use in recombinant TIMP-3 prodn. Genes coding for TIMP may also be useful for gene therapy e.g. of emphysema. Sequence 820 BP; 204 A; 225 C; 188 G; 203 T;
                                                                                                                                                                                                   New tissue inhibitor metallo:proteinase cancer, inflammation, emphysema, embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T02360;
29-FEB-1996
                                                                                                                                                                                                                                                                                       04-OCT-1994; U11241.
06-OCT-1993; US-134231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIMP-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T02360 standard;
                                                                                                                                                                                                                                    P-PSDB; R84216
                                                                                                                                                                                                                                                 WPI; 95-155259/20.
                                                                                                                                                                                                                                                                          (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                  WO9509918-A1.
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               Similarity
                                                                                Genes coding for TIMP may also be useful
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5.7%;
larity 60.9%;
Conservative
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                                                       227 A;
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0; Mismatc
Score 60;
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re 60; DB 16; Le
1. No. 4.93e-20;
Mismatches 107;
                                                       276 C;
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4.93e-20;
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                                                     229 T;
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atggcaatatgcatatcaccctctgtgacttcatcgtgccctgggacaccctgagtgcca

Qy	B	Qy	DЪ	Qy	망	ΟУ	탕
884	531	824	471	764	411	704	351
884 gctcctgcgcctggtaccgcggagcagcacccc 917	531 getaetgeagetggtaeegaggatgggeeeece 564	cggagaagaacatcaacggacaccaggccaagttcttcgcctgcatcaagagaagcgacg 883	471 ccaatttcggttaccctggctaccagtccaaacactacgcctgcatccggcagaagggcg 530	764 gcccatgatcccatgctacatctcctctccggacgagtgcctctggatgga	411 gctactacctgccttgctttgtgacttccaagaacgagtgtctctggaccgacatgctct 470	704 cccagaagaagagcctgaaccacaggtaccagatgggctgtgagtgcaagatcactcgat 763	cccagcgcaaaggggctgaactatcggtatcacctgggttgtaactgcaagatcaagtcct 410

Search completed: Mon May 4 13:25:12 1998 Job time: 375 secs.

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	(MT)

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MPsrch_nn :no on: n.a. n.a. database search, using Smith-Waterman algorithm

llar output not generated. Mon May 4 12:33:57 1998; MasPar time 1070.95 Seconds 1186.262 Million cell updates/sec

Description: Perfect Score: N.A. Sequence: >006583 (1-1045) from n-geneseq.seq 1045

1 attccggcttctatggagca......ctggacacagcatgaataaa 1045 taaggccgaagatacctcgt.....gacctgtgtcgtacttattt

Scoring table: TABLE default Gap 6

Nmatch

STD:

Searched: 1610801 seqs, 607859669 bases x 2

Dbase 0; Query 0

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: embl-est

1:em_est1 2:em_est2 3:em_est3 4:em_est4 5:em_est5 6:em_est6 7:em_est8 8:em_gss 9:em_est13 genbank-est

Database:

10:gb_est1 11:gb_est2 12:gb_est3 13:gb_est4 14:gb_est5 15:gb_est6 16:gb_est7 17:gb_est8 18:gb_est9 19:gb_est10 20:gb_est11 21:gb_sts 22:gb_gss 23:gb_est12 24:gb_est13 25:gb_est14 26:gb_est15 27:gb_est16 28:gb_est17 29:gb_est18 30:gb_est19 31:gb_est20

tistics: Mean 10.886; Variance 2.366; scale 4.602

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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293 272	315	325 322	326	351 344	364 354	400	Score
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16 12	16	18 24	29	18 25	16 28	28	DB.
W49721 R68697	W49694 W49722	AA183676 AA462734	AA700818	AA183361 AA486280	W49684 AA400168	AA400097	Ħ
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C18912 T50035 T50090 AA754459	MMB614 AA505775 AA702765	AA542611 AA518518 W11774 AA234603	R22149 AA323024 MUSGS00647 C01506 R22150	AA286368 R26961 T29410 T54278 T48827 R24085	AA627637 T54386 T53334 W11897 R68647	M85579 M85403 T53335 AA369501 AA364950
Human placenta cDNA 5' yb04h03.r2 Homo sapien yb04h03.s1 Homo sapien 97SN1787 Rice Immature	mRNA (c NCI_CG! Soares	1111	.rl Homo 6 Cerebe 3'-direc 08501, H	· · ·	. 51 . 51	Homo Homo 1 Ho Plac
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		⊅	ALIGNMENTS		
RESULT 1	AA400097	556 bp	mRNA	EST	09-NOV-1997
DEFINITION	zu69f08.sl similar to	Soares testis NHT gb:S48568 TISSUE 1	<pre>zu69f08.s1 Soares testis NHT Homo sapiens cDNA clone 743271 3' similar to gb:S48568 TISSUE INHIBITOR OF METALLOPROTEINASES II precursor (HMMAN):</pre>	Homo sapiens cDNA clone 743271 INHIBITOR OF METALLOPROTEINASES	ne 743271 3' OTEINASES II
ACCESSION					
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens	Metazoa:	Homo sapiens Rukarvotae: Metazoa: Chordata: Vertebrata: Mammalia:	rata: Mammali	a: Eutheria:
REFERENCE	Primates; C	atarrhini;	Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 556)	•	
AUTHORS	Hillier,L., Krizman,D.,	Allen,M., Kucaba,T.	<pre>Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,</pre>	que,T., Geise , Lennon,G.,	el,G., Jost,S., Marra,M.,
	Theising, B., White, Y., Wyli	, White, Y.	Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R	rston, R. and	Wilson, R.
JOURNAL	Unpublished (1997)	(1997)			
	Contact: Wilson RK	lson RK	. a-table at works		
	Washington 4444 Forest Tel: 314 28 Fax: 314 28	ington University Forest Park Park 314 286 1800 314 286 1810	Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810	ine t. Louis, MO	63108
	Email: est@watson.wustl.edu This clone is available rov	iwatson.wus is availab	<pre>This clone is available rovalty-free through LLNL ;</pre>	through LLNL	contact the
	IMAGE Consortium (insert Length: 869	ortium (inf jth: 869	IMAGE Consortium (info@image.llnl.gov) for further Insert Length: 869 Std Error: 0.00) for further	
	Seq primer:	-41m13 fw	Seq primer: -41m13 fwd. ET from Amersham	ham	
FEATURES	M Trenh uhru	Location/Qualifiers	Location/Qualifiers		
source		1556			
	> >	ote="Vecto	organism="Homo sapiens" onte="Vector: pT7T3D-Pac (Pi	harmacia) wit	h a modified
	ď.	olylinker;	polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand	ite_2: Eco RI	; 1st strand cDNA

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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                ccctgcaatgagatactccttctttcctccaatgtccagcgagaccccacacacggcagc 571
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g1337958
EST.
                                                                                                                                  zc43c09.rl Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 325072 5' similar to gb:S48568 TISSUE INHIBITOR OF METALLOPROTEINASES II PRECURSOR (HUMAN);
Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; H
1 (bases 1 to 518)
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/clone="743271"
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/sex="male"
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                                                                  GGGTCACAGAGAAGAACATCAACGGGCACCAAGGCCAAGTTCTTCGCCTGCATCAAGAGA
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agcgacggctcctgcgcctggtaccgcggagcagcacccccaagcaggagtttctggac
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WashU-Merck EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 314 286 1800 Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                     n 34.8%;
Similarity 89.6%;
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Seq primer: mob.REGA+ET
High quality sequence stop: 381.
Location/Qualifiers
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/tlssue_type="senescent fibroblast"
/lab_host="DH10B (ampicillin resistant)"
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/clone="325072"
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                                                  ACCCTATCAAGAGGATCCAGTATGAGATCAAGCAGATAAAGATGTTCAAAGGGCCTGAGA 278
AGGATATAGAGTTTATCTACACGGCCCCCCCCCCCGGCAGTGTGTGGGGGTCTCGCTGGACG 338
                               accccatcaagcggattcagtatgagatcaagcagataaagatgttcaagggacctgatc 538
                                                                                                                                                                             389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 869 Std Error: 0.00
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 493.
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1 (bases 1 to 583)

Hiller,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost
Hillaran,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
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Fax: 314 286 1810
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larity 91.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dub
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; M
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                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
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                                                           organism="Mus musculus"/strain="Inbred CD-1"
sex-"males"
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Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
Tel: 314 286 1800
                                                                         1 (bases 1 to 467)
Hillier,L., Allen,M., Bowles,L., Dubuque,T.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F
White,Y., Wylie,T., Waterston,R. and Wilson,
Washd-Merck EST Project 1997
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Vertebrata; Mammalia;
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                                                                        zi69f06.s1 Soares fetal liver spleen clone 436067 3' similar to gb:S48568 METALLOPROTEINASES II PRECURSOR (HUMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41m13 fwd. ET from Amersham
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/lab_host="SOLR (kanamycin resistant)"
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                                                                                                                                                                                                                                                                                   Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jos Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylle, T., Waterston, R. and Wilson, R. Washu, NCI human EST Project
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Fax: 314 286 1810
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/note="Organ: Liver and Spleen; Vector: pT/T3D (Pharmacia)
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/lab_host="DH10B (ampicillin resistant)"
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ACCCCATCAAGAGGATTCAGTATGAGATCAAGCAGATAAAGATGTTCAAAGGACCTGACA 377
                                                                            tgatcagggccaaagcagtcaataagaaggaggtggactctggcaacgacatctacggca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., D
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. an
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                                                                                                                                                             423;
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Washbr-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. L
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High quality sequence stop: 444.
Location/Qualifiers
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Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
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Vertebrata; Eutheria;
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The WashU-HHMI Mouse EST Project
                                                                                                                                                                                  Similarity
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llarity 84.1%;
Conservative
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                                                                                                                                                                                                                                                             /dev_stage="10-12 week old"
/lab_host="SOLR (kanamycin resistant)"
<1. .>757
<198 c 210 g 163 t 2 oth
                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
/clone="567758"
                                                                                                                                                                                                                                                                                                                                              /sex="males"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Mus musculus"/strain="Inbred CD-1"
                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Stratagene mouse testis (#937308)"
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Pred. No. 0.00e+00;
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Marra, M.; Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuc, Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
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AA462734
92187625
                                                                                                                                                                    Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further:
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
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The WashU-HHMI Mouse EST Project
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314 286 1810
             /organism="Mus musculus"
/strain="C57BL/6J"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand was primed with a Not I - oligo(dT) primer [5'
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Eutheria; Primates; C
1 (bases 1 to 434)
Hillier, L., Clark, N.,
                                                                                                  human clone=70287 library=Stratagene placenta (#937225)
vector=pBluescript SK- host=SOLR cells (Kanamyoin resistant)
primer=M13RP1 Rsitel=EcoRI Rsite2=XhoI Placental tissue from a
Caucasian male. Cloned unidirectionally. Primer: Oligo dT. Average
insert size: 1.2 kb; Uni-ZAP XR Vector; 5' adaptor sequence:
5'-GARTTCGGCACGAG-3', 3' adaptor sequence:
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larity 88.8%;
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/clone_lib="Soares mouse
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                                   Catarrhini;
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Pred. No. 0.00e+00;
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Dubuque, T.,
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Unpublished (1995)
Other_ESTs: yb05d08.s1
Contact: Wilson RK
WashU-Merck EST Project
Washington University Sch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High qality sequence stops: 391
Source: IMAGE Consortium, LLNL;
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
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Tel: 314 286 1800
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Parsons,J., Rifkin,L., Rohlfing,T.,
Waterston,R., Williamson,A., Wohldm
                                                                                         zc43c09.s1 Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 325072 3' similar to gb:S48568 TISSUE INHIBITOR OF METALLOPROTEINASES II PRECURSOR (HUMAN);.
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Fax: 314 286 1810
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Similarity 90.0%;
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                Homo sapiens
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
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Wohldmann,P. and Wilson,R.
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GTGTCCCAGGGCACGATGAAGTCACAGAGGGTGATGTGCATCTTGCCGTCCCCCTCGGCC
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WashU-Merck EST Project
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Hillier,L., Clark,N., Dubuque,T., E.
Holman,M., Hultman,M., Rucaba,T., L.
Parsons,J., Rifkin,L., Rohlfing,T.,
                                                                                                                                                                                                                                                                                                                                                                                                       403;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
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Similarity 88.2%;
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Location/Qualifiers
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/clone="325072"
/clone_lib="Soares senescent fibroblasts NbHSF"
/tissue_type="senescent fibroblast"
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Pred. No. 0.00e+00;
0; Mismatches 47
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ctgt----caattggccccaggagtcctggtggcctgcttacgggtcctcgatgtccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 577
                                                                                                                         ch 30.1%;
l Similarity 88.2%;
403; Conservative
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WashU-Merck EST Project
Washington University So
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 489)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soarse,M., Tan,F., Parsons,J., Rifkin,L., Rohlfing,T., Soarse,M., Tan,F., Parsons,J., Waterston,R., Williamson,A., Wohldmann,P. and
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/tissue_type="senescent fibroblast"
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METALLOPROTEINASES II PRECURSOR (HUMAN);.
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4444 Forest Park Parkway,
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Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 327)

Hilller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                 CDNA was ligated to Eco RI adaptors (pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.
                                                                                                                                                                                                                                 Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Os Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia;
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                                                                                                                                                     Homo sapiens
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/tissue_type="senescent fibroblast"
/lab_host="DH10B (ampicillin resistant)"
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The WashU-Merck EST |
----nhlished (1995)
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EST.
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High quality sequence stops: 187
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@inage.llnl.gov) for further i
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Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Ostsarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Eutheria; Archonta; Primates; Catarrhini; Hominidae; H. (bases 1 to 394)

1 (bases 1 to 394)

Adams, M.D., Dubnick, M., Kerlavage, A.R., Moreno, R., Kellyterback, T.R., Magle, J.W., Fields, C. and Venter, J.C. Sequence identification of 2,375 human brain genes

Nature 355 (6361), 632-634 (1992)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                     human clone=HFBCK35 library=Fetal brain, Stratagene (cat#936206) vector=LambdaZAP-II primer=M13 Forward 17-18 wk gestation, femal oligo-dT + random primed cDNA synthesis; lambdaZAP-II vector, 1.
                                                                                                                                                                                                                                                    Metalloproteinase
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/clone="139180"
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Adams,M.D., Dubnick,M., Kerlavage,A.R., Moreno,R., Ke Utterback,T.R., Nagle,J.W., Fields,C. and Venter,J.C. Sequence identification of 2,375 human brain genes Nature 355 (6361), 632-634 (1992)
                                                                                                                                                                                                                                                                    EST01918 Homo sapiens cDNA clone HFBCH66 similar to Metalloproteinase inhibitor. M85403
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                                                                                                 Eukaryotae: Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomía; Chordata; Vertebrata; Gnathostomata; Ost
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Ho
                                                                                                                                                               Homo sapiens
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932 Clopper Road, Gaithersburg, MD 20
Tel: 3018699056
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Human melanoma cell line A2058
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IRAKAVSEKEVDSGNDIYGNPIKRIQYEIKQIKMFKGPEKDIEFIYTAPSSAVCGVSL
DVGGKKEYLIAGKABGDGKNHITICDFIVPWDTLSTTQKKSLNHRYQMGCECKITRCP
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                                                                                                                                                                                                                                                                                                                                                                                                                 'gene-"TIMP"
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                                                                                                                                                                                                                                                                                                                                                                                                  'note="metalloproteinase-2
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l. No. 0.00e+00;
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Best Local Similarity
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                                               GGGGTCTCGCTGGACGTTGGAGGAAAGAAGGAATATCTCATTGCAGGAAAGGCCGAGGGG
                                                                                                 TTCAAAGGGCCTGAGAAGGATATAGAGTTTATCTACACGGCCCCCTCCTCGGCAGTGTGT
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This sequence comes from 6-7
Location/Qualifiers
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IRAKAVSEKEYDSGNDIYGNPIKRIQYEIKQIKMFKGPEKDIEFIYTABSSAVCGVSL
DVGGKKEYLIAGKAESGKMHITICDDIYPMDTLSTTQKKSLMHRYQMCGCKITTCK
MIPCYISSPDECLMMDWVTEKNINGHQAKFFACIKRSDGSCAMYRGAAPPKQEFIDIE
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                Submitted (08-SEP-1994) N.C. Partridge, School of Medicine, Department of Pharm. South Grand, St. Louis, MO 63104, USA
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Cook,T.F., Burke,J.S.,
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Rattus norvegicus
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Evertebrata; Eutheria; Rodentia; Sciurognathi; N
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/product="tissue inhibitor of metalloproteinases-2"
/db_xref="PID:9540205"
/db_xref="PID:9540205"
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MIPCYISSPDECLMMDWVTEKSINGHQAKFFACIKRSDGSCAMYRGAAPPKQEFLDIE
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/cell_line="UMR 106-01 rat osto
/cell_type="osteoblast"
/tissue_type="bone"
                                                                                                                                                                                                                          /strain="Sprague-Dawley"
/db_xref="taxon:10116"
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Purification, cDNA cloning, and developmental changes in the steady-state mRNA level of rat testicular tissue inhibitor
                                                                                                                                                                                  Eukaryotae;
Vertebrata;
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/db_xref="pid:918814"
/db_xref="pid:91881814"
/trans!ation="MGAAARSLRLALGLLLLATLLRPADACSCSPVHPQQAFCNADVV
/trans!ation="MGAAARSLRLALGLLLLATLLRPADACSCSPVHPQQAFCNADVV
IRAKAVSEKEVDSGNDYSQNPIKRIQYEIKQIKMFKGPDKDIEFIYTAPSSAVCGVSL
DVGGKKEYLIAGKAEGDGKMHITLCDFIVPMDTLSITQKKSLNHRYQMGCECKITRCP
MIPCYISSPDECLMMDMVTEKSINGHQAKFFACIKRSDGSCAWIRGAAPPKQEFLDIE
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219. .881
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/product="tissue inhibitor of metalloproteinase type 2"
/db_xref="piD:9619233"
/translation="MGAAARSIRLAIGILILATILRPADACSCSPVHPQQAFCNADVV
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Mus musculus (strain BALB/c, sub_species lambda gtil) embryo cDNA to mRNA.
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Shimizu, S., Malik, K.,
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                                                                                                                                                                                          extracellular protein; matrix metalloproteinase inhibitor; tissue
                                                                                                                                                                                                                                      mRNA,
                                                                         Koiwai,O
                                                                                                           Murinae; Mus.
                                                         sequence of mouse TIMP-2
                                                                                                                                                                                                                                   complete
                     Location/Qualifiers
1. .1695
/organism="Mus musculus"
/strain="BALB/c"
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                                                                                  Sejima, H.,
                                                                                                                                                                                                                                             (type 2)
                                                                                                                                                                                                                                                                       mRNA
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                                                                                  Kishi,J.,
                                                                                                                                                                                                                                                                      ROB
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                                                                               Hayakawa,T.
                                                                                                                   Myomorpha;
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                                                                                                                    Muridae;
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295. .876
/gene="TIMP2"
/product="tissue:
969. .974
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/note="putative;
a 515 c 468
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217. .879
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/tissue_lib="lambda gtll"
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/cell_type="fibroblast"
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/db_xref="taxon:10090"
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90.7%;
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Pred. No. 0.00e+00;
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inhibitor of matrix metalloproteinases; TIMP-2
inhibitor of metalloproteinases, Type 2.
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92290292
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x62622 S37984
 58.9%;
Similarity 90.7%;
700; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shimizu, S., Malik, K., Sejima, H., Kishi, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (14-OCT-1991) S. Shimizu, Pathophysiology Unit, Aichi
Cancer Center Research Institute, 1–1 Kanokoden, Chikusa-ku, Nav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shimizu, S.
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Vertebrata; Eutheria; Rodentia; Sciurognathi; N
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ene 114 (2), 291-292 (1992)
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305. .886
                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/strain="BALB/c"
                                                                                                       product="mature Tissue
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                        Boone,T.C., Johnson,M.J., De Clerck,Y.A. and Langley,K.E. CDNA cloning and expression of a metalloproteinase inhibitor related to tissue inhibitor of metalloproteinases proc. Natl. Acad. Sci. U.S.A. 87, 2800-2804 (1990)
                                                                                           Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Artiodactyla; Ruminantia; Pecora;
Bovidae; Bovinae; Bos.
                                                                                                                                                  metalloproteinase inhibitor.
Bovine aorta endothelium, cD
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aggagtttctcgacatcgaggacccataagcaggcctccaacgcccctgtggccaactgc
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                               AGGAGTTTCTGGACATCGAGGACCCGTAAGCAGGCCACCAGGACTCCTGGGGCCCAATTG-
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                                                          TTGCAGGGAAGGCCGAGGGGAATGGCAATATGCATATCACCCTCTGTGACTTCATCGTGC 684
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350 /
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1042. .1047
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/db_xref="taxon:9913"
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                                                                                                      l Similarity
691; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gibbons, K.L., O'Grady, R.L. and Piper, A.A. Rat tissue inhibitor of metalloproteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 matrix metalloproteinase inhibitor. Rattus norvegicus (tissue library:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus
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Vertebrata; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1994)
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larity 90.8%;
Conservative
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                                                                                                                                                                           /product="matrix metalloproteinase
869. 958
297 c 288 g 169 t
                                                                                                                                                                                                                                                                                          /translation="MGAAARSIRLALGILLLATLLRADACSCSPVHPQQAFCNADVV
IRAKAVSEKEVDSGNDIYGNPIKRIQYEIKQIKMFKGPDKDIEFIYTAPSSAVCGVSL
DVGGKKEYLIAGKAEGDGKMHITLCDFIVPWDTLSITQKKSLNHRYQMGCECKITRCP
MIPCYISSPDECLWMDWVTEKSINGHQAKFFACIKRSDGSCAWTRGAAPPKQEFLDIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="TIMP-2"
209. .286
                                                                                                                                                                                                                                                                   287. .868
                                                                                                                                                                                                                       /function="tissue (type 2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="mammary"
/tissue_lib="lambda gt1
                                                                                                                                                                                                                                                    /gene="TIMP-2"
                                                                                                                                                                                                                                                                                                                                                      /product="matrix metalloproteinase inhibitor"
/db_xref="PID:g1141730"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cell_type="carcinoma"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                         'codon_start=1
'function="tissue inhibitor of matrix metalloproteinase
                                                                                                                                                                                                                                                                                                                                                                                                                               'gene="TIMP-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          'gene="TIMP-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism≈"Rattus norvegicus"
db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
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Eutheria; Rodentia; Sciurognathi; N
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Differential regulation of TIMP-1 and TIMP-2 mRNA normal and Ha-ras-transformed murine fibroblasts Gene 117, 209-217 (1992) 92347695
                                                                                                                                                                                                                                                          metalloproteinase inhibitor. (metalloproteinase inhibitor. )
                                                                                                                                                                                                                                                 Mus musculus (strain Mus musculus
                                                                                                                                                                                                                                                                                                                        M.musculus metalloproteinase inhibitor (TIMP-2)
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Vertebrata; Eutheria; Rodentia; Sciurognathi; N
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/strain="c3H"
/db_xref="taxon:10090"
/cell_line="C3H 10T1/2"
/cell_type="fibroblasts"
                                                                                       Location/Qualifiers
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/db_xref="PID:9202054"
/db_xref="PID:9202054"
/translation="MGAAARSLRLAHGLLLASLLRPADACSCSPVHPQQAFCNADVV
/translation="MGAAARSLRLAHGLLLLASLLRPADACSCSPVHPQQAFCNADVV
IRAKAVSEKEVDSGNDIYGNPIKRIQYEIKQIKMEKGPDKDIEFIYTAPSSAVCGVSL
DVGGKKEYLIAGKAEGDGKMHITLCDFIVPWDYLSITQKKSLNHRYQMGCECKITRCP
MIPCYISSPDECLMMDWVTEKSINGHQAKFFACIERSDGSCAWYRGAAPPKQEFLDIE
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                                                                                                                                                                    TACACGGCCCCCTCCTCGGTAGTGTGTGGGGTCTCACTGGACGTTGGAGGAAAGAAGAA
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                          atcgtgccctgggacaccctgagcaccaccagaagaagagcctgaaccacaggtaccag
                                            ATCGTGCCCTGGGACACCCTGAGCACCACCCAGAAGAAGAGCCTGAACCACGGTACCAG
                                                                                         tatctcattgcaggaaaggccgaggggacggcaagatgcacatcaccctctgtgacttc
                                                                                                                                                      tacacggccccctcctcggcagtgtgtggggtctcgctggacgttggaggaaagaaggaa
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Malik,K., Sejima,H., Aoki,T. and Iwata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H.sapiens mRNA for tissue inhibitor of metalloproteinases, Type-2.
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Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147
                                                                                                                                                                                                                                                                                                                                                                                                              52.3%;
llarity 98.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="TIMP-2"
547. .555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="cloning primer-derived (3')"
148 c 159 g 101 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FFACIKRSDGSCAWYRGAAPPKQEF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PWDTLSTTQKKSLNHRYQMGCECKITRCPMIPCYISSPDECLWMDWVTEKNINGHQAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="SPVHPQQAFCNADVVIRAKAVSEKEVDSGNDIYGNPIKRIQYEI
KQIKMFKGPEKDIEFIYTAPSSVVCGVSLDVGGKKEYLIAGKAEGDGKMHITLCDFIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cell_line="GIN-1"
/clone_lib="human fibroblast"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="TIMP-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="Tissue inhibitor of metalloproteinases, /db_xref="PID:g37181" /db_xref="SWISS-PROT:p16035"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="TIMP-2"
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Pred. No. 0.00e+00;
0; Mismatches 7
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Takaoka City, Toyama 933, Japan
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primer_bind
primer_bind
mat_peptide
BASE COUNT 10
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AUTHORS
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Best Local S
Matches 54
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    448
              126 ATCAAGAGGATCCAATATGAGATCAAGCAGATAAAGATGTTCAAAGGCCCTGACAAAGAC
                                                         388
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                                                                   AGGGCCAAAGCAGTAAGCGAGAAGGAGGTGGATTCCGGGAACGACATCTACGGCAACCCC
                                                                                                                        GCCTGCAGCTGCCCCCGGTGCACCCGCAACAGGCGTTTTGCAATGCAGACGTAGTGATC
                                                                                                           gcctgcagctgctccccggtgcacccgcaacaggcgttttgcaatgcagatgtagtgatc
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atcaagaggatccagtatgagatcaagcagataaagatgttcaaagggcctgagaaggat
                                                       agggccaaagcggtcagtgagaaggaagtggactctggaaacgacatttatggcaaccct
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Tissue i
                                                                                                                                                                      546;
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Cricetulus longicaudatus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (02-NOV-1993) Y. Suzuki, Suntory Pharm-Tech Cen 370-05 Akaiwa 2716, Chiyoda-machi, Ohra-gun, Gumma, JAPAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                         1. .35
9. .590
9. .590
a 163
                                                                                                                                                                                                                                                                                             /product="tissue inhibitor of metaro proteinase"
/db_xref="piD:9414877"
/db_xref="piD:9414877"
/translation="RACSCSPVHPQQAFCNADVVIRAKAVSEKEVDSGNDIYGNPIKR
IQYEIKQIKMFKGPDKDIEFITTAPSSAVCGVSLDVGGKKEYLIAGKAEGDGKMHITL
CDFIVPWDTLSTTQKKSLNHRYQMGCECKITRCPMIPCYISSPDECLWMDWVTEKSIN
GHQAKFFACIKRSDGSCAWYRGAAPPKQEFLDIEDP"
                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Cricetulus longicaudatus"
/db_xref="taxon:10030"
/clone_lib="chinese hamster ovary"
/clone="K1"
                                                                                                                                                                                                                                                                                                                                                                                                              /cell
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93.2%;
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                                                                                                                                                                 Score 506; DB 14;
Pred. No. 0.00e+00;
0; Mismatches 40
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GCCCGCCGTCCCCACCCCGCCGCCCCGCCCGGCGAATTGCGCCCCGCGCCCCCTCCCCTC 635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ctctqtgacttcatcgtgccctgggacaccctgagcaccacccagaagaagacctgaac
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                                                                                                                                                                                                                                                                                                                                                   GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 143852] from the original journal article. This sequence comes from Fig. 1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       timp-2-metalloproteinase-2 tissue inhibitor {promoter} {human,
Genomic, 970 nt].
                           oh 36.4%;
L Similarity 100.0%;
376; Conservative
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                                                                                                                                                 'codon_start=1
                                                                                                                                                               /gene="timp-2"
                                                                                                                                                                                /partial
                                                                                                                                                                                                             /note="metalloproteinase-2 tissue inhibitor"
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                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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                                                                                                                                    translation="MGAAARTLRLALGLLLLATLLRPADACSCSPVHPQQAFCNADVG"
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                           Score 376; DB 28;
Pred. No. 3.96e-240;
0; Mismatches 0;
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                                                      Length 970;
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g2352472
                                                                                                                                                                                                                                                                                 Submitted (17-MAY-1997) University of California - San Diego, Department of Chemistry and Biochemistry, 9500 Gilman Drive, Jolla, CA 92093-0654, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus (TIMP-2) mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aimes, R.T., Li, L., Weaver, B., Hawkes, S., Cloning, expression and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                  Phasianidae; Phasianinae; Gallus.
1 (bases 1 to 814)
Aimes, R.T., Li, L., Weaver, B., Haw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chicken.
Gallus gallus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata, Vertebrata; Archosauria; Aves; Neognathae; Galliformes;
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          /translation="MPGAALPSLLAWLAVLLLGRARPADACSCSPIHPQQAFCNADVV
IRAKRYSAKEYDSGNDIYGNPIKRIQYEYKQIKMFKGPDQDIEFIYTAPSTEYCGQPL
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                                                                    precursor"
                                                                                  /function="matrix metalloproteinase inhibitor"
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/product="tissue inhibitor of metalloproteinase-2
                                                                                                                                               /gene="TIMP-2"
17. .679
                                                                                                                                                                        ...814
SIPCFVSSSDECLWTDWAMEKIVGGRQAKHYACIKRSDGSCAWYRGMAPPKQEFLDIE
                                                                                                                                                                                      /dev_stage="10
                                                                                                                                                                                                                                                                ocation/Qualifiers
                                                                                                                              gene-"TIMP-2"
                                                                                                                                                                                                           'clone="3"
                                                                                                                                                                                                                       db_xref="taxon:903"
                                                                                                                                                                                                                          organism="Gallus gallus"
/dh wref="taxon:9031"
                                                      'db_xref="PID:g2352473"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tissue inhibitor
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Best Local Similarity 79.7%;
Matches 484; Conservative
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                                                                     856 gcgtggtaccgcggcgcgcgcccccaagcaggagtttctcgacatcgaggacccataa 915
                                                                                        620 GCCTGGTACCGCGGCATGGCCCCCCCGGAAGCAGTTTCTCGACATCGAGGACCCCTAA 679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="TIMP-2"
95. .676
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Search completed: Mon May 4 14:13:19 1998 Job time: 2867 secs.

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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

: no r ular output not generated. Mon May 4 14:13:39 1998; MasPar time 1063.28 Seconds 1181.104 Million cell updates/sec

Description:
Perfect Score:
N.A. Sequence:
Comp: 1033 >Q06584
(1-1033) from n-geneseq.seq

Title:

Scoring table: 1 attccggccgccgtccccc......aacactcatccccggaattc 1033 taaggccgggcggcaggggg.....ttgtgagtaggggccttaag

Mmatch STD: TABLE default Gap 6 Dbase 0; Query 0

1610801 seqs, 607859669 bases x 2

Minimum Match 0% Listing first 45 summaries

Database: embl-est Post-processing:

Searched:

1:em_est1 2:em_est2 3:em_est3 4:em_est4 5:em_est5 6:em_est6 7:em_est8 8:em_gss 9:em_est13 genbank-est

Database:

10:gb_est1 11:gb_est2 12:gb_est3 13:gb_est4 14:gb_est5 15:gb_est6 16:gb_est7 17:gb_est8 18:gb_est9 19:gb_est10 20:gb_est11 21:gb_est8 22:gb_gs 23:gb_est12 24:gb_est13 25:gb_est14 26:gb_est15 27:gb_est16 28:gb_est17 29:gb_est18 30:gb_est19 31:gb_est20

itistics: Mean 10.965; Variance 2.456; scale 4.464

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	n		ი	a	a	o.				a	_		a	
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Score	545	463	459	448	438	436	425	385	385	373	365	360	346	
Query Match	52.8	44.8	44.4	43.4	42.4	42.2	41.1	37.3	37.3	36.1	35.3	34.8	33.5	
Length DB	556	518	467											
D8	28	16	25	29	16	16	28	10	16	10	18	12	28	
Ħ	AA400097	W49684	AA486280	AA700818	W49694	W49722	AA400168	T48826	W49721	T53335	AA183361	M85579	AA627637	
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1.66e-201 1.03e-199 1.03e-199	4.07e-223 2.60e-221 4.27e-214	0.00e+00 2.82e-29 4.08e-25	0.00e+00	0.00e+00	0.00e+00 0.00e+00 0.00e+00	0.00e+00	0.00e+00 0.00e+00	0.00e+00 0.00e+00	0.00e+00	0.00e+00	0.00e+00

ALIGNMENTS

FEATURES Source	TITLE JOURNAL COMMENT	REFERENCE	DEFINITION ACCESSION NID KEYWORDS SOURCE ORGANISM	RESULT 1 LOCUS
Contact: Wilson KK Washington University School of 4444 Forest Park Parkway, Box 85 Tel: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty. IMAGE Consortium (info@image.lin Insert Length: 869 Std Error: Seq primer: -41ml3 fwd. E7 from High quality sequence stop: 473. Location/Qualifiers 1. 556 /organism="Homo sapiens /note="Vector: p1713D-P polylinker; Site_1: Not	Martin, J., Moore, B., Schell Theising, B., White, Y., Wyli WashU-NCI human EST Project Unpublished (1997)	Eukaryotae; Primates; Ca 1 (bases 1 Hillier,L., Krizman D	zu69108.sl S zimilar to g PRECURSOR (H AA400097 g2053962 EST. human.	AA400097
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wilson kk st Park Parkway, Bo 286 1810 286 1810 286 1810 tewatson.wustl.edu e is available roya sortium (info@image ngth: 869 Std Err r: -41m13 fwd. ET f ity sequence stop: Location/Qualifiers Location/Qualifiers /organism="Homo sap polylinker; Site_1:	., sche. ,Y., Wy. T. Projec	a; Choreni; Hom;) M., Bow	testis NHT 568 TISSUE	m qd
Contact: Wilson KK Washington University School of Medicine Washington University School of Medicine Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu Email: est@watson.wustl.edu Email: est@watson.wustl.edu Info@image.linl.gov) for further Insert Length: 869 Std Error: 0:00 Seq primer: -41ml3 fwd. E7 from Amersham High quality sequence stop: 473. Location/Qualifiers 1. 556 /organism="Homo Sapiens" /note="Yector: p773D-Pac (Pharmacia) with polylinker; Site_1: Not I; Site_2: Eco RI;	Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Washd-NCI human EST Project Unpublished (1997)	Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalla; Eu Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 556) Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Krizman D. Knoaba T. Lary M. Lennon G. Marra	ZU69T08.s1 Soares testis NHT Homo sapiens CDNA CLORE /432/1 similar to gb:S48568 TISSUE INHIBITOR OF METALLOPROTEINASES PRECURSOR (HUMAN); AA400097 g2053962 EST. EST. Homo sapiens	mRNA
St. Louis, MO 6 St. Louis, MO 6 sthrough LLNL; phorfurther sham sham sham site_2: Eco RI;	Steptoe, M. Ston, R. an	ita; Mamma ie,T., Gei	ENS CDNA CON METALLO	EST
Contact: wilson kk Washington University School of Medicine Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 fel: 314 286 1810 Email: est@watson.wustl.edu Ensail: est@watson.wustl.edu Insert Length: 869	d Wilson, R.	Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 556) Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman D. Kucaba T. Lacv M. Le N. Lennon,G. Marra,M.	HOMO SAPIENS CDNA CLONE /432/1 3'	09-NOV-1997

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Local Similarity 97.3%;
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                                                              GCACCAGCAGAAGAAGAGCCTGAACCACAGGTACCAGATGGGCTGCGAGTGCGAAGATCA 240
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gggtcacagagaagaacatcaacgggcacca-ggccaagttcttcgcctgcatcaagaga
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WashU-Merck EST Project
WashIngton University School of Medi
4444 Forest Park Parkway, Box 8501,
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Parsonskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Insert Length: 615 Std Error: 0.00
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Fax: 314 286 1810
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/db_xref="taxon:9606"
/clone="325072"
/clone="325072"
/clone_lib="Soares senescent fibroblasts NDHSF"
/tissue_type="senescent fibroblast"
/lab_host="DH10B (ampicillin resistant)"

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                                                                                              466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -41ml3 fwd. ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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llarity 99.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              zi69f06.s1 Soares fetal liver spleen 1NFLS clone 436067 3' similar to gb:S48568 TISSUE METALLOPROTEINASES II PRECURSOR (HUMAN);.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WashU-NCI human EST
Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40ml3 fwd. ET from Amersham.
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Washington University Sch
4444 Forest Park Parkway,
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Email: est@watson.wustl.edu
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WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
Tel: 314 286 1800
                                                                                                                                  Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Home 1 (bases 1 to 489)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                         2C43C09.sl Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 325072 3' similar to gb:S48568 TISSUE INHIBITOR OF METALLOPROTEINASES II PRECURSOR (HUMAN);
                                                                                             The WashU-Merck EST Unpublished (1995)
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/lab_host="DH10B (ampicillin resistant)"
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/sex="male"
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/clone="436067"
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/tissue_type="senescent fibroblast"
/lab_host="DH108 (ampicillin resistant)"
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WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. /
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Hiller, L., Clark, N., Dubugue, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
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/clone="325120"
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Local Similarity 100.08;
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                                                                                     425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insert Length: 869    Std Error: 0.00
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 493.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 869 Std Error: 0.00
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jos
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                            went through one round of normalization to Cot5, ar
constructed by Bento Soares and M. Fatima Bonaldo
/db_xref="GDB:5930425"
                                                                                                                                                                                                                                                                                                                                                                      Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT/T3 vector. Library
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/sex="male"
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/clone="743271"
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                                                                                                                                                              Contact: Wilson RK
WashU-Merck EST Project
WashIngton University Schoo
4444 Forest Park Parkway, B
Tel: 314 286 1800
Pax: 314 286 1810
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1 (bases 1 to 434)

Hillier.L., Clark, N., Dubuque, T., Elliston
Holman, M., Hultman, M., Kucaba, T., Le, M., I
Parsons, J., Rikin, L., Rohlfing, T., Tan, F.

Williamson, A., Wohldmann, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                        human clone=70287 library=Stratagene placenta (#937225)
vector=pBluescript SK- host=SOLR cells (kanamycin resistant)
primer=M13RP1 Rsite1=EcoRI Rsite2=XhoI perimer: tissue from a
Caucasian male. Cloned unidirectionally. Primer: Oligo dT. Average:
insert size: 1.2 kb; Uni-ZAP XR Vector; 5' adaptor sequence:
5'-GAATTCGGCACGAG-3'; 3' adaptor sequence:
                                                                                                                                                                                                                                                          Waterston, R., Williamson, A., WashD-Merck EST Project Unpublished (1995).
Other_ESTs: yb05d08.s1
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                                                                                                                                              Email: est@watson.wustl.edu
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ce: IMAGE Consortium, LLNL
clone is available royalty-free through LLNL;
E Consortium (info@image.llnl.gov) for further;
           /organism="Homo sapiens"
/clone="70287"
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Catarrhini; Hominidae;
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           Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Insert Length: 627 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality second
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                                                                                                                                                                                                                        Vertebrata; Eutheria; Primates; Calai....., Vertebrata; Eutheria; Primates; Calai....., 1 (bases 1 to 532)
Hillier,L., Clark,N., Dubuque,T., Elliston, Holman,M., Hultman,M., Kucaba,T., Le,M., Le Parsons,J., Rifkin,L., Rohlfing,T., Soares, Waterston,R., Williamson,A.,
                                                                                                                                                                                                                                                                                                                                                                                             zc43g09.rl Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 325120 5' similar to gb:s48568 TISSUE INHIBITOR OF METALLOPROTEINASES II PRECURSOR (HUMAN);.
                                                                                           WashU-Merck EST Project
WashIngton University School of Medicine
WashIngton Parkway, Box 8501, St. I
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                               Contact: Wilson RK
                                                                                                                                                                                            Unpublished
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Vertebrata;
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llarity 97.4%;
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Location/Qualifiers
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No. 0.00e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       485;
human clone=68727 library-Stratagene placenta (#937225)
vector=pBluescript SK- host=SOLR cells (kanamycin resistant)
primer=-21mi3 Rsitel=EcoRI Rsite2-KhoI Placental tissue from a
Caucasian male. Cloned unidirectionally. Primer: Oligo dT. Average
                                                                                                                ya88b08.s1 Homo sapiens cDNA clone 68727 3' similar to gb:S48568 TISSUE INHIBITOR OF METALLOPROTEINASES II PRECURSOR (HUMAN).
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llarity 95.7%;
Conservative
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/clone="325120"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Soares senescent fibroblasts
/tissue_type="senescent fibroblast"
/lab_host="DH10B (ampicillin resistant)"
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407; Conser
                          mo96g07.rl Stratagene mouse testis (#937308) Mus musculus cDNA clone 567612 5' similar to gb:S48568 TISSUE INHIBITOR OF METALLOPROTEINASES II PRECURSOR (HUMAN); gb:X62622 M.musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Source: IMAGE Consortium, LLNL this clone is available royalty free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WashU-Merck EST Project
Washington University Sch
4444 Forest Park Parkway,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WashU-Merck EST Project
Unpublished (1995)
Other_ESTs: ya88b08.rl
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Eutheria; Primates; Catarrhini; Hominidae;
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5'-GAATTCGGCACGAG-3'; 3' adaptor sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5'-CTCGAGTTTTTTTTTTTTTTTT-3'
AA183361
              TIMP-2 mRNA for tissue inhibitor of metalloproteinases, (MOUSE);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
High qality_sequence stops:
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llier,L., Clark,N., Dubuque,T.,
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llarity 97.4%;
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/clone="68727"
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Local Similarity 88.4%;
hes 443; Conservative
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CTAATTGCAGGAAAGGCAGAAGGAGATGGCAAAGATGCACATTACCCTCTGTGAGCTTCATT
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                                                                                                                                                                                                                                                                                                                                                         acggccccctcctcggcagtgtgtggggtctcgctggacgttggaggaaagaaggaatat
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EST.
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School of MedicineP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The WashU-HHMI Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
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/clone="567612"
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/strain="Inbred CD-1"
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Pred. No. 0.00e+00;
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                                                                                                           61 AAGAGCCTGAACCACAGGTACCAGATGGGCTGCGGATGCAAGATCACGCGCTGCCCCATG 120
                                                                                                                                                                          1 ATGCACATCACCCTCTGTNACTTCATCGTGCCCTGGGACACCCTGAGCACCCACCCAGAAG
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AACATCAACGGGCACCAGGCCAAGTTCTTCGCCTGCATCAAGAGAAGTGACGGCTCCTGT
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                            aagagcctgaaccacaggtaccagatgggctgcgagtgcaagatcacgcgctgccccatg
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                                                                                                                                                                                                                            386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Kerlavage AR
The Institute for Genomic Research
932 Clopper Road, Gaithersburg, MD 20
Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human clone-HFBCK35 library-Fetal brain, Stratagene (cat#936206) vector-LambdaZAP-II primer-M13 Forward 17-18 wk gestation, female; oligo-dT + random primed cDNA synthesis; lambdaZAP-II vector, 1.0kb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adams,M.D., Dubnick,M., Kerlavage,A.R., Mc
Utterback,T.R., Nagle,J.W., Fields,C. and
Sequence identification of 2,375 human bra
Nature 355 (6361), 632-634 (1992)
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Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; H
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Similarity 97.7%;
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Location/Qualifiers
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/gene="D0S272E"
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/clone="HFBCK35"
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Pred. No. 0.00e+00;
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1 Similarity 96.8%;
363; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nq51c01.s1 NCI_CGAP_Co10 Homo sapiens similar to gb:S48568 TISSUE INHIBITOR
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                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trace considered overall poor quality Seq primer: -40ml3 fwd. ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRECURSOR (HUMAN);.
AA627637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tissue Procurement: Ilan Kirsch, M.D., Michael R.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
Tumor Gene Index
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Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                    /note-*Organ: colon; Vettor: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from RER+ colon tumor, and was then primed with a Not I coligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo (N-Soares4)."
                                                                                                   /clone="IMAGE:1147392"
/clone_1ib="NCI_CGAP_CO10"
/tissue_type="colon tumor RER+"
/lab_host="DH10B"
96 c 127 g 98 t
                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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    Score 346; DB 28;
Pred. No. 0.00e+00;
0; Mismatches 11
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OF METALLOPROTEINASES
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EST.
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubu Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vf91a09.rl Soares mouse mammary gland NbMMG Mus musculus cDNA clone 851128 5' similar to gb:X62622 M.musculus TIMP-2 mRNA for tissue
                                                                                                                                                                                                                                                                           Contact: Marra M/Mouse EST Project
Washbr-HHMI Mouse EST Project
Washbryton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                           The WashU-HHMI Mouse EST Project 
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
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AA462734
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High quality sequence stop: 369.
Location/Qualifiers
                                                                                                                                                                                           This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               house mouse.
                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
             386
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double-stranded cDNA was ligated to Eco
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l (bases 1 to 757)
Marra, M., Hillier, L., Alle Geisel, S., Kucaba, T., Lacy Schellenberg, K., Steptoe, M Theising, B., Wylie, T., Len Waterston, R.
                                                                                                                                                                                               mo98c08.rl Stratagene mouse testis (#937308) Mus musculus cDNI clone 567758 5' similar to gb:S48568 TISSUE INHIBITOR OF METALLOPROTEINASES II PRECURSOR (HUMAN); gb:X62622 M.musculus TIMP-2 mRNA for tissue inhibitor of metalloproteinases, (MOUS)
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Eukaryotae;
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Conservative
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/dev_stage="4 weeks"
/lab_host="DH10B"
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the Not I and Eco RI sites
RNA provided by Dr. Minoru
constructed and normalized
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/clone="851128"
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Pred. No. 0.00e+00;
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                                                       Allen, M.,
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This clone is available royalty-free t
IMAGE Consortium (info@image.llnl.gov)
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WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
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Search completed: Mon May 4 14:42:31 1998 Job time: 1732 secs.

Searched:	Scoring table:	Title: Description: Perfect Score: Sequence:	ular output not generated.	MPsrch_pp prote	Release Copyrig	
120837 segs, 14945562 residues	PAM 150 Gap 11	>R07954 (1-220) from a-geneseq.pep 1651 1 mgaaarslplafcllllgtlcawyrgaappkqefldiedp 220	Mon May 4 14:49:00 1998; MasPar time 9.43 Seconds 348.668 Million cell updates/sec	protein - protein database search, using Smith-Waterman algorithm	Release 3.0.5AA John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1997 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd	(TW)

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq31
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
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24:part24 25:part25 26:part26

Statistics: Mean 31.999; Variance 118.552; scale 0.270

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 1651 100.0 220 12 R07954 2 1651 100.0 220 2 R07954 3 1550 93.9 220 12 R65769 4 1550 93.9 220 12 R07995 6 1416 85.8 194 2 R06898 7 1365 82.7 186 2 R06898 8 1339 81.1 192 2 R06899 8 1339 81.1 192 2 R06897 10 817 49.5 224 23 R925603 11 815 49.4 224 18 R92565 12 702 42.5 211 25 W30310 13 681 41.2 211 12 R84215 14 681 41.2 211 13 R65002 18 668 40.5 188 25 W30308 19 669 40.5 211 13 R65001	Result	Score
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                         New metallo-proteinase inhibitor polypeptide(s) - and DNA encoding them, for treatment of tumour cell dissemination and rheumatoid arthritis

Claim 12; Fig 1; 63pp; English.

The product has therapuetic use in inhibiting tumour dissemination during chemotherapy and radiation therapy, impurged bone marrow cell harvesting etc. The inhibitor may also be useful in encapsulating tumours aiding clean excision, and in treatment of enphysema, Paget's disease, osteoporosis, scleroderma and bedsores.

The gene product also has application in autoimmune disorders eg. The umatoid arthritis and multiple sclerosis.

See also Q06584.
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EP-398753-A.
22-NOV-1990.
Human metalloproteinase inhibitor,
Metalloproteinase inhibitor; tumour cell dissemination;
rheumatoid arthritis; dystrophic epidermolysis bullosa;
emphysema; osteoporosis; MI gene disorders.
                                                                            R62769 standard;
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(CHIL-) CHILDREN'S HOSPITAL OF LA.
LANGLEY KE, BOODE TC. Declerck YA;
LANGLEY KE, BOODE TC. Declerck YA;
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scleroderma; cholesteatoma.
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Tumour; chemotherapy; cancer; Paget's disease; osteoporosis;
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19-MAY-1989; US-355027.
29-MAR-1990; US-501904.
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                                                                                                                                                                                                                                                                                                                                                                      220 AA;
                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers 27..220
                                                                             Protein;
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                                                      entry)
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                                                                                                                                                                                                                                                                                                                    Score 1651; DB 2;
Pred. No. 3.28e-173;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                         Length 220;
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R WPI; 95-098775/13.

"I New human tissue inhibitor of metallo:proteinase-3 - used to "I develop prods. for diagnosis, therapy or prophylaxis of conditions with unwanted matrix metallo:proteinase activity. Disclosure; Fig 6A-B; 87pp; English.

"The protein sequence of human TIMP-2 is compared with the cattle, protein sequence of human TIMP-1, mouse and cattle TIMP-2, and chicken (Ch) and mouse TIMP-1, mouse and cattle TIMP-2, and chicken (Ch) and mouse TIMP-3. A probe based on the ChIMP-3 can be used to isolate DNA encoding comino acid sequence (R65000) is used to isolate DNA encoding thuman TIMP-3 from a human CDNA library. Human TIMP-3 can be used to the diagnosis, therapy or prophylaxis of conditions characterized by excess or unwanted matrix metalloproteinase conditions."
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Best Local
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                                                                                                                                                         23-FEB-1995.
12-AUG-1994; U09188.
12-AUG-1993; US-105263.
13-DEC-1993; US-167463.
(REGC) UNIV CALIFORNIA.
Hawkes SP, Kishnani NS,
WPI; 95-098775/13.
                                                                                                                                                                                                                                                                                       treating tumour cell dissemination, rheumatoid arthritis and for large-scale recombinant inhibitor prodn.

Claim 8; Fig 2; 65pp; English.

Q73088 encodes R62769 human metalloproteinase inhibitor (MI), it may be used to inhibit tumour cell dissemination and for treating rheumatoid arthritis, dystrophic epidermolysis bullosa, emphysema and osteoporosis. The DNA may be used to detect MI gene disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; Q73088.

New metallo:proteinase inhibitor, analogues and DNA -
                                                                                                                                                                                                                                                                                prophylaxis.
                                                                                                                                                                                                                                                                                                                                                  R65009
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(AMGE-) AMGEN INC.
(CHIL-) CHILDRENS HOSPITAL LOS ANGELES
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; US-355027.
; US-501904.
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                                                                                                                                                                                                                                                                                        of metalloproteinase; diagnostic; therapeutic
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                                                                                                                                                                      Yang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1550; DB 12;
Pred. No. 1.40e-161;
12; Mismatches 6;
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Best Local
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18-MAY-1990; :
19-MAY-1989; !
29-MAR-1990; !
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Sequence 220 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            during chemotherapy and radiation therapy, impurged bone marrow contains the control of the cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   See also Q06583.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New metallo-proteinase inhibitor polypeptide(s) - and DNA encoding them, for treatment of tumour cell dissemination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Langley KE. Boone TC, DeClerck WPI; 90-350481/47.
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Tumour; chemotherapy; cancer; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R07955;
21-FEB-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The product has therapuetic use in inhibiting tumour dissemination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AMGE-) AMGEN INC.
(CHIL-) CHILDREN'S HOSPITAL
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Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                   1550; DB 2;
No. 1.40e-161;
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                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
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Best Local S
Matches 18
Synthetic.
US7494796-A.
21-AUG-1990.
                                                                                                                                                                                                                                                                                                                                                                                                             the amino acid sequence determined. A probe was synthesised based upon the protein sequence information. It was used to screen a LambdaGem-4 cDNA library prepared from human melanoma cells. 239 positives were identified from a total of 750,000 plaques screened Further analysis and screening with additional probes eliminated most of the clones. Clone pSS38 was isolated and the nucleotide sequence of the cDNA insert was determined. The deduced amino acid sequence showed excellent agreement with that derived by directly sequencing the TIMP-2 protein.

See also 005937, R06746-R06750, R06894-R06895 and Q05938-Q05939.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JUL-1989;
18-AUG-1989;
13-MAR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (USSH ) NAT INST OF HEALTH.
Stetler-Sevenson WG, Liotta LA,
WPI; 90-290097/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 matrix metalloproteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnosis, detection and purificn..
Disclosure; F1g 7; 54pp; English.
TIMP-2 was isolated from human melanoma cell-conditioned media and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R06898
                                     matrix metalloproteinase inhibitor;
                                                Part of TIMP-2
                                                                            R06896;
                                                                                        R06896
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New matrix metallo-proteinase inhibitor - used to resulting from matrix metallo-proteinase activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R06898;
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                                                              l6-JAN-1991 (first entry)
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                                                                                                                                       aappkqefldiedp 194
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aappkqefldiedp 220
                                                                                                                                                                                                                                                                                            ryqmgceckitrcpmipcyisspdeclwmdwvtekninghqakffacikrsdcscawyrg
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                                                                                                                                                                                           ryqmgceckitrcpmipcyisspdeclwmdwvtekninghqakffacikrsdgscawyrg
                                                                                        standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence of
                                                                                                                                                                                                                                                                                                                                                                                                       194 AA;
                                                                                                                                                                                                                                                                                                                                                  85.8%;
larity 93.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-494796
                                     metalloproteinase inhibitor, encoded
proteinase inhibitor; TIMP-2; pSS15.
                                                                                      protein; 186 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   humam TIMP-2 f nase inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194
                                                                                                                                                                                                                                                                                                                                                  Score 1416; DB 2;
Pred. No. 3.58e-146;
9; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Krutzsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from clone
r; TIMP-2; |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
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                                                                                                                                                                                                                                                                                                                                                                           Length 194;
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and in
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R06895;
R06895;
DT 16-AN-1991 (first entry)
DE Metalloproteinse inhibitor TIMP-2.

EN Matrix metalloproteinase inhibitor; TIMP-2 (
OS Synthetic.

PN US7494796-A.

PN US7494796-A.

PR 13-MAR-1990; 494796.

PF 13-MAR-1990; US-326334.

PR 17-JUL-1989; US-380431.

PR 17-JUL-1989; US-380431.

PR 18-AGG-1999; US-395453.

PR 13-MAR-1990; US-494796.

PR (USSH ) NAT INST OF HEALTH.

PI Stetler-Sevenson WG, Liotta LA, Krutzsch HC;

PR WET; 90-29097/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnosis, uccerring the problem of the amino acid sequence determined. A probe was synthesised the amino acid sequence determined. A probe was synthesised based upon the protein sequence information. It was used to screen a LambdaGem-4 cDNA library prepared from human melanoma cells. 239 positives were identified from a total of 750,000 plaques screened. Further analysis and screening with additional probes eliminated all but two clones (pSSI5 and pSSI8). Both were sequenced and found to encode CSC-21K (-TIMP-2), a novel metalloproteinase inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-MAR-1990; 494796.
21-MAR-1989; US-326334.
17-JUL-1989; US-380431.
18-AUG-1989; US-395453.
13-MAR-1990; US-494796.
            New matrix metallo-proteinase inhibitor - used to treat diseases resulting from matrix metallo-proteinase activity and in diagnosis, detection and purificn.. Disclosure; Fig 5; 54pp; English.

Protein was isolated from human melanoma cell-conditioned media gelatin-affinity chromatography.

It inhibits matrix metalloproteinases and can be used to treat diseases such as arthritis, diabetes, cancer, ulcers of mucosa a diseases such as arthritis, diabetes, cancer, ulcers of mucosa a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pss15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (USSH ) NAT INST OF HEALTH. Stetler-Sevenson WG, Liotta WPI; 90-290097/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnosis, detection and purificm...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New matrix metallo-proteinase inhibitor - resulting from matrix metallo-proteinase a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; Q05938
                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       also Q05937, R06746-R06750, R06894-R06895 and Q05939-Q05940.
uence 186 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            kitrcpmipcyisspdeclwmdwvtekninghqakffacikrsdgscawyrgaappkqef 180
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larity 94.1%;
Conservative
 autoimmune-mediated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1365; DB 2;
Pred. No. 2.58e-140;
10; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. No. 2.58e-
Mismatches
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                                                                                                                                                                                                                                                                                                   TIMP-2

    used to
    activity

 inflammation,
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(
                                                                                                                                                                                                                                                                                                 (CSC-21K).
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                                                                                                    treat diseases and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treat diseases
lung
             mucosa and
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                                                                                                                                                                                      Query Match
Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                 They matrix metallo-proteinase inhibitor - used to treat diseases in resulting from matrix metallo-proteinase activity and in it diagnosis, detection and purificn.

Disclosure; Fig 6B; 54pp; English.

TIMP-2 was isolated from human melanoma cell-conditioned media and the amino acid sequence determined. A probe was synthesised based upon the protein sequence information. It was used to screen a LambdaGem-4 cDNA library prepared from human melanoma cells. 239 positives were identified from a total of 750,000 plaques screened. Further analysis and screening with additional probes eliminated all but two clones (pSS15 and pSS18). Both were sequenced and found to encode CSC-21K (-TIMP-2), a novel metalloproteinase inhibitor.

This is the amino acid sequence deduced from the cDNA sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 17
                                                                                                                                                                                                                                                                                                  See also Q05937,
Sequence 177 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-JAN-1991 (first entry)
Part of TIMP-2 metalloproteinase inhibitor, encoded matrix metalloproteinase inhibitor; TIMP-2; pSS18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            granulomatous diseases and myocardial infarctions. It can also be used as a birth control agent by preventing embryo/placental attachment or invasion. Other therapeutic benefits may also be obtd. in diseases with basement destruction or myocyte destruction. See also Q05937, R06746-R06750, R06894 and Q05938-Q05940.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 90-290097/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (USSH ) NAT INST OF HEALTH.
Stetler-Sevenson WG, Liotta LA, Krutzsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-MAR-1990; 494796.
21-MAR-1989; US-326334.
17-JUL-1989; US-380431.
18-AUG-1989; US-395453.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; Q05939.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-MAR-1990; US-494796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R06897
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aappkqefldied 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aappkqefldied
                                                                                                                                                                                           167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                      78.8%;
larity 94.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                        R06746-R06750,
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90.7%;
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                                                                                                                                                                                      Score 1301; DB 2;
Pred. No. 5.69e-133;
8; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1339; DB 2;
Pred. No. 2.49e-137;
10; Mismatches 7;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIMP-4 can be used to treat disorders associated with excessive metalloprotease expression, e.g. tumour metastasis, anglogenesis and growth, osteoarthritis, osteoprosis, pulmonary emphysema, periodontal disease and rheumatoid arthritis, and for contraception. TIMP-4 CDNA can be used for gene therapy of such disorders and in diagnostic assays for TIMP-4 mRNA in cells and tissues. Oligonucleotide fragments of the TIMP-4 CDNA and antagonists or inhibitors of TIMP-4 can be used to treat disorders associated with over-expression of TIMP-4, e.g. to promote healing of corneal and diabetic ulcers and ulcers/lesions caused by microorganisms. Antibodies to TIMP-4 can be used to diagnose such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding a tissue inhibitor of metallo:proteinase(s), TIMP-4 for production of recombinant protein for treating tumours, arthritis, etc., and for contraception Claim 1; Fig 1; 24pp; English.

This sequence is a tissue inhibitor of metalloproteinases designs TIMP-4. The cDNA clone was identified with Incyte Clone No. 5893
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Tissue inhibitor of metalloproteinase, TIMP-4; Incyte Clone No. 589345;
Tissue inhibitor of metalloproteinase; TIMP-4; Incyte Clone No. 589345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (INCY-) INCYTE PHARM INC. Hawkins PR, Murry LE; WPI; 97-350238/32.
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d. No. 8.97e-78;
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Claim 14; Fig 1; 49pp; English.
Human tissue inhibitor of metalloproteinase-4 (TIMP-4) (R98265)
Is a novel member of the TIMP family. Its amino acid sequence was deduced from a cDNA clone (T34433) obtd. from an early stage human brain. The sequence shows 40% identity to human TIMP-2.
Recombinant TIMP-4 can be expressed in e.g. E. coll, COS or insect cell hosts. It can be used to treat patients in need of TIMP-4 (e.g. cancer, arthritic diseases, bone resportion diseases, Paget's disease, hyperparathyroidism and cholesteatoma), and to screen for antagonists useful for treating patients in need of TIMP-4 inhibition (e.g. for tissue repair and remodeling). It can also be used in
                                                                                                                                                                                                                                                                                                        29-JAN-1998 (first entry)
Human TIMP-1/TIMP-3 fusion protein.
TIMP-3; human; antibody; TIMP-3-mediated disease; malignant tumour cell;
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                                                                             Misc-difference
                                                                                                                                                                                                                                                               cancer progression; TIMP-1.
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WPI; 96-300644/30.
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13-DEC-1994;
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R98265;
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pred. No. 1.51e-77;
58; Mismatches 58
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Example 12; Page 34-35; 37pp; Japanese.

This sequence represents a fusion protein between the human TIMP-1 and TIMP-3 proteins. This sequence was used to test the specificity of the connoclonal antibody (MAD) of the invention. The MAD of the invention reacts specifically with human TIMP-3 (see W30308), by specific recognition of the TIMP-3 fragments represented by W30305-W30307. The MAD can be used in the study or diagnosis of TIMP-3-mediated diseases, can be used in the study or diagnosis of TIMP-3-mediated diseases, can be used for the detection of malignant tumour cells, or the castablishing an immunoassay for TIMP-3 or in purification of TIMP-3. The transformed cells can be used for producing TIMP-3 or its equivalent proteins on a large scale. The immunoassay method for TIMP-3 the MADs is simple, highly reproducible and highly sensitive.
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The product (R84216) of Timp3clone2 cDNA clone (T02360) is a natural variant of the Timp3clone7 clone product (R84215), lacking part of the signal peptide. The product, TIMP-3, is a novel tissue inhibitor metalloproteinase. Recombinant TIMP-3 be expressed in prokaryotic or eukaryotic host cells and used the control of the con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIMP-3 clone-2 product.
TIMP-3; tissue inhibitor metalloproteinase type three; inflammation; emphysema; embryo implant modulation; art
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R84216 standard; Protein; 198
R84216;
                                                                                                                                                                                                                                  New tissue inhibitor metallo:proteinase cancer, inflammation, emphysema, embryo
                                                                                                                                                                                                                                                                                               N-PSDB; T02360
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WPI; 95-155259/20.
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06-OCT-1993; US-134231.
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Pred. No. 8.56e-65;
54; Mismatches 57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      develop prods. for diagnosis, therapy or prophylaxis of conditions with unwanted matrix metallo:proteinase activity. Disclosure; Fig 11: 87pp; English.

Human TIMP-3 can be used for the diagnosis, therapy or prophylaxis of conditions characterized by excess or unwanted matrix metalloproteinase activity, e.g. neoplasias, tunor metastasis, inflammatory disorders such as rheumatoid arthritis, ulcerations, reaction to infection, periodontal disease or osteoporosis. It can also be used in drug screening/design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hawkes SP, Kishnan
WPI; 95-098775/13.
N-PSDB; Q82747.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-AUG-1993; US-105263.
13-DEC-1993; US-167463.
(REGC) UNIV CALIFORNIA.
Hawkes SP, Kishnani NS,
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Tissue inhibitor
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                                                                                                                                                                                                                                                                                                                                                              similarity 43.78;
87; Conservative
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51; Mismatch
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Pred.
51; M
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. No. 1.97e-62;
Mismatches 51;
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L.97e-62;
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Best Local Similarity 43.7%;
Matches 87; Conservative
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R84215 standard; Protein; 211 AA.
R84215;
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TIMP-3 clone-7 product
TIMP-3 tlssue inhibitor metalloproteinase type three; cancer;
inflammation; emphysema; embryo implant modulation; arthritis;
dystrophic epidermolysis bullosa; peridontal disease; ulcer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and used to
Sequence 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The product (R84215) of Timp3cione7 cDNA clone (T02359) is a novel tissue inhibitor metalloproteinase, designated TIMP-3. Recombinant TIMP-3 can be expressed in prokaryotic or eukaryotic host cells and used to treat degradative diseases of connective tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-APR-1995.
04-OCT-1994; U11241.
06-OCT-1993; US-134231.
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Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AMGE-) AMGEN INC.
Koski RA, Silbiger SM;
WPI; 95-155259/20.
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202 awyrgaappkqefldiedp 220
                                                             193 swyrgwappdkslinatdp 211
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ell disorders, etc.
laim 3; Page 66-67; 112pp; English.
he product (R84215) of Timp3clone7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tissue inhibitor metallo:proteinase type three - for treating per, inflammation, emphysema, embryo implant modulation, nerve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 681; DB 15; Length 211; Pred. No. 1.97e-62; 51; Mismatches 51; Indels 1
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Search completed: Mon May 4 14:49:28 1998 Job time: 28 secs.

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Release 3.0.5AA John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1997 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

: no on: bular output not generated. Mon May 4 14:46:56 1998; MasPar time 8.66 Seconds 637.128 Million cell updates/sec

Description: Perfect Score: Sequence:

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Scoring table: PAM 150 Gap 11 >R07954
(1-20) from a-geneseq.pep
1651
1 mgaaars1plafc1111gt1.....cawyrgaappkqefldiedp 220

Searched: 69112 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 44.292; Variance 65.300; scale 0.678

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	5.4.4	5.4	5.5	6.1	6.2	29.4	30.5	30.5	30.8	30.8	31.0	31.0	31.0	40.3	40.7	40.7	41.2	41.2	93.0	93.6	93.9	100.0	Query Match
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	PPOL_HUMAN	PPOL_XENLA	POL3_DROME	YATR_BACFI	YBD7_YEAST	TIM1_PIG	TIM1_RAT	TIM1_MOUSE	TIM1_SHEEP	TIM1_RABIT	TIM1_HUMAN	TIM1_PAPCY	TIM1_BOVIN	TIM3_RAT	TIM3_MOUSE	TIM3_BOVIN	TIM3_CHICK	TIM3_HUMAN	TIM2_MOUSE	TIM2_RAT	TIM2_HUMAN	TIM2_BOVIN	IJ.
•	POLY (ADP-RIBOSE) POLY (ADP-RIBOSE)	_	RETROVIRUS-RELATED POI	HYPOTHETICAL ABC TRANS	ALPHA-ADAPTIN HOMOLOG	METALLOPROTEINASE	Description																
	POLY	POLY	TOP	TRANS	8	IHII	IHII	IHI	IHII	IHI	IHI	IHI	IHII	IHI	IHI	IHNI	IHII	IHII	IHII	IHI	IHI	IHI	
	4.03e-01	4.03e-01	2.81e-01	6.27e-03	1.89e-03	1.28e-96	1.83e-101	9.83e-102	8.19e-103	8.19e-103	1.27e-103	1.27e-103	6.82e-104	5.98e-146	1.33e-147	1.33e-147	8.22e-150	4.35e-150	0.00e+00	0.00e+00	0.00e+00	0.00e+00	Pred. No.

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RA54_YEAST	YHZ7_YEAST	HFE1_HAEIN	DNAJ_STRCO	TRPA_SYNY3	POL2_DROME	SP97_HUMAN	NUOL_RHOCA	DHA7_YEAST	INO1_CITPA	CPBC_RAT	YRS4_CAEEL	NODC_RHILP	YOBX_MYCTU	IPGB_SHIDY	ECP_RAT	REP2_ZYGFE	PPOL_BOVIN	HYPB_ECOLI	LUXP_VIBHA	ABL1_HUMAN	ABL_MOUSE
DNA REPAIR AND RECOMBI	HYPOTHETICAL 86.7 KD P	MINOR FIMBRIAL SUBUNIT	DNAJ PROTEIN.	TRYPTOPHAN SYNTHASE AL	RETROVIRUS-RELATED POL	PRESYNAPTIC PROTEIN SA	NADH DEHYDROGENASE I C	POTASSIUM-ACTIVATED AL	MYO-INOSITOL-1-PHOSPHA	CYTOCHROME P450 IIB12	HYPOTHETICAL 49.4 KD P	N-ACETYLGLUCOSAMINYLTR	HYPOTHETICAL 38.0 KD P	IPGB PROTEIN.	EOSINOPHIL CATIONIC PR	TRANS-ACTING FACTOR C	POLY (ADP-RIBOSE) POLY	HYDROGENASE ISOENZYMES	LUXP PROTEIN PRECURSOR	PROTO-ONCOGENE TYROSIN	PROTO-ONCOGENE TYROSIN
3.31e+00	3.31e+00	3.31e+00	3.31e+00	3.31e+00	1.67e+00	2.35e+00	2.35e+00	1.67e+00	2.35e+00	2.35e+00	1.67e+00	1.67e+00	1.67e+00	2.35e+00	1.67e+00	1.17e+00	8.25e-01	5.78e-01	8.25e-01	4.03e-01	4.03e-01

ALIGNMENTS

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PIR; A35922; A3 PIR; A34468; A3 PIR; A34468; A3 PROSITE; PS0028 METALLOPROTEASE SIGNAL CHAIN DISULFID	MURRAY J.B., ALLISON K., J. BIOL. CHEM. 261:4154- [3] SEQUENCE OF 27-71. MEDLINE: 90008914. DE CLERCK Y.A., YEAN T.D J. BIOL. CHEM. 264:17445 -1- FUNCTION: COMPLEXES AND IRREVERSIBLY INA -1- PTM. THE ACTIVITY OF DISULFIDE BONDS: -1- SIMILARITY: HIGH WIT EMBL, M32303; G163342; EMBL, M32303; G163342;	TIMP2. BOS TAURUS (BOVIN BUKARYOTA; METAZO EUTHERIA; ARTIODA [1] SEQUENCE FROM N.A MEDLINE; 90207285 BOONE T.C., JOHNS BROC. NATL. ACAD. [2] SEQUENCE OF 27-71 TISSUE-CARTILAGE;	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
96; A3596. 96; A3596. PS00284 FIMP; 1. OTEASE INHIBITOR; 20 27 29 27 29 154 29 154 201 172 193 159 164	LINE; 86140235. BIOL. CHEM. 261:4154-4159(1986). BIOL. CHEM. 261:4154-4159(1986). DIENCE OF 27-71. LINE; 90008914. CLERCK Y.A., YEAN T.D., RATZKIN B BIOL. CHEM. 264:17445-17432(1989). BIOL. CHEM. 264:17445-17432(1989). FUNCTION: COMPLEXES WITH METALLO. AND IRREVERSIBLY INACTIVATE THEM. PTM. THE ACTIVITY OF TIMP-2 IS D DISULFIDE BONDS. SIMILARITY: HIGH WITH OTHER MEMB L; M32303; G163342;	URUS (BOVINE). (COTA; METAZOA; CHORDATA; RIA; ARTIODACTYLA. RCE FROM N.A. RE; 90207285. T.C., JOHNSON M.J., DE NATL. ACAD. SCI. U.S.A. RCE OF 27-71. S-CARTILAGE;	ANDAR 15, 18, 31, 31, INHI
SI	T.D., RATZKIN B.J. A43-17453(1986). T.D., RATZKIN B.J. A43-17453(1989). ES WITH METALLOPRO ES WITH METALLOPRO OF TIMP-2 IS DEPE WITH OTHER MEMBERS;	ATA; DE C	REATED) AST SECTION 2 CTOR 2 COLLAGE
GNAL. METALLOPROTEINASE BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY.	., LANGEI .J., LU I .PROTEINA EPPENDENT	EBRATA; K Y.A., 800-2804	PRT; 220 AA.
E INHIBITOR	R R.; H.S., LANGLEY K. ISES (SUCH AS COL ON THE PRESENCE)DA;	-2) (TISSUE
N	(K.E.; COLLAGENASES) ENCE OF	MAMMALIA;	INHIBITOR OF

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      RAC RAPARAL RANGE 
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Best Local S
Matches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE; 90207285. BOONE T.C., JOHNSON PROC. NATL. ACAD. S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIM2_HUMAN STANDARD; PRT; 220 AA. P16035; 093006; 01-APR-1990 (REL. 14, CREATED) 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE) 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) METALLOPROTEINASE INHIBITOR 2 PRECURSOR (TIMP-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
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                                                                                                                                                                               SEQUENCE OF 27-219.
MEDLINE; 90008902.
STETLER-STEVENSON W.G., KRUTZSCH H.C.,
J. BIOL. CHEM. 264:17374-17378(1989).
                                                                                                                                                                                                                                                                                                                                                                     TISSUE-PLACENTA;

MEDLINE; 96411768.

HAMMANI K., BLANIS A., MORSETTE D., BOWCOCK

HENRIET P., DECLERCK Y.A.;

J. BIOL. CHEM. 271:25498-25505(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE; 90338014.
STEPLER-STEVENSON W.G., BROWN P.D.,
J. BIOL. CHEM. 265:13933-13938(1990)
                                                                                 MEDLINE; 90046765.
MCDLINE; 90046765.
GOLDBERG G.I., MARMER B.L., GRANT G.A.,
PROC. NATL. ACAD. SCI. U.S.A. 86:8207-8
                                                                                                                                                                                                                                                                                        SEQUENCE OF 30-214 FROM N.A.
MALIK K., SEJIMA H., AOKI T., IWATA K.;
SUBMITTED (AUG-1990) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METALLOPROTEINASES-2) (CSC-21K).
                                       EQUENCE OF 27-41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
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ISSUE-SYNOVIAL FLUID;
EDLINE; 92111776.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
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                                                                      ATL. ACAD.
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56
68
220
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larity 100.0%;
Conservative
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56
68
24355
                                                                              S.A.
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                                                                      GRANT G.A., EISEN A.Z.,
A. 86:8207-8211(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1651;
Pred. No. 0.
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                                                                                                                                                                                                       LIOTTA L.A.;
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CRC32;
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.00e+00;
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                                                                                                  MILHELM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIOTTA L.A.;
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Best Local
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- I SIMILARITY: HIGH WITH OTHER MEMBERS OF THE TIMP FAMILY.

EMBL; J0593; G339707; -.

EMBL; S48568; G298202; -.

EMBL; U44385; G1517893; -.

EMBL; U44382; G1517893; JOINED.

EMBL; U44382; G1517893; JOINED.

EMBL; U44382; G1517893; JOINED.

EMBL; U44383; G1517893; JOINED.

EMBL; U44383; G37181; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OSTHUES A., KNAUEPER V., (
FEBS LETT. 296:16-20(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FREEDMAN R.B., FEENEY J.;
BIOCHEMISTRY 33:11745-11759(1994).
-i- FUNCTION: COMPLEXES WITH METALLOPROTEINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
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-!- PTM: THE ACTIVITY OF TIMP-2 IS DEPENDENT ON THE PRESENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WILLIAMSON R.A.,
121
                                                                                                                                                                                      121
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                                                                                                                                                                                                                                                                                                                                                        188825;
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larity 91.8%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OF 27-153.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ₩.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAT -> P (IN REF. 3).

M -> K (IN REF. 5).
P -> I (IN REF. 5).
A -> V (IN REF. 5).
S -> E (IN REF. 5).
M -> R (IN REF. 5).
M -> R (IN REF. 5).
M -> Q (IN REF. 5).
M -> T (IN REF. 5).
M -> T (IN REF. 5).
M -> T (IN REF. 5).
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1550; DB 1; |
Pred. No. 0.00e+00;
12; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 220;
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RESULT TO AC PO

TIM2_RAT P30121; 01-APR-1993

STANDARD;

PRT;

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(REL. 25, CREATED)

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Best Local :
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EMBL; U14526; G540205; --
EMBL; U14528; G5141730; --
EMBL; S72594; G619233; --
EMBL; S82718; G1881814; --
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ROSWIT W.T., MCCOURT D.W., PARTRIDGE N.C., JEFFREY J.J.;

RACH. BIOCHEM. BIOPHYS. 292:402-410(1992).

-i- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)

-i- PIM: THE ACTIVITY OF TIMP-2 IS DEPENDENT ON THE PRESENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SANTORO M., BATTAGLIA C., ZHANG I SALVATORE D., FUSCO A.; EXP. CELL RES. 213:398-403(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-SPRAGUE-DAWLEY; TISSUE-BONE; MEDLINE; 94263207.

COOK T.F., BURKE J.S., BERGMAN K.D. PARTRIDGE N.C.;

PARCH. BIOCHEM. BIOPHYS. 311:313-320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
METALLOPROTEINASE INHIBITOR 2 PRECURSOR (TIMP
METALLOPROTEINASES-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=MAMMARY;
GIBBONS K.L., C
                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; S20325; S20325
PROSITE; PS00288; T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 27-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 96384329.
GRIMA J., CALCAGNO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE; 94326839.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBMITTED (JUN-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIMP2 OR TIMP-2
                                                                                                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METALLOPROTEASE
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    61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFIDE BONDS
                                                                                                      MGAAARSLRLALGLLLLATLLRPADACSCSPVHPQQAFCNADVVIRAKAVSEKEVDSGND
                 IYGNPIKRIQYEIKQIKMFKGPDKDIEFIYTAPSSAVCGVSLDVGGKKEYLIAGKAEGDG 120
                                                                                iygnpikriqyeikqikmfkgpdqdiefiytapaaavcgvsldiggkkeyliagkaegng
                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                         153
220
                                                                                                                                                                    93.6%;
llarity 92.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O'GRADY R.L., PIPER A.A.;
N-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                           ă,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INHIBITOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIMP; 1.
                                                                                                                                                                                                                                                         153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZHANG L.,
                                                                                                                                                                  Score 1546; DB 1; Lei
Pred. No. 0.00e+00;
Pred. No. 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL.
                                                                                                                                                                                                                                                                         BY SIMILARITY.
CONTROL OF CONTROL 
                                                                                                                                                                                                                                                                                                                                                                                                                                                       METALLOPROTEINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRECURSOR (TIMP-2)
                                                                                                                                                                                                                                                           222F8EDA
                                                                                                                                                                                                                                                       > T (IN REF. 1).
> Q (IN REF. 1).
22F8EDA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARLOMAGNO F., MARTELLI M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                c.o.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THE TIMP FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                         INHIBITOR
                                                                                                                                                                                                             Length 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JEFFREY J.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TISSUE INHIBITOR
                                                                                                                                                                       Indels
                                                                                                                                                                    0;
                                                                                                                                                                       Gaps
                                                                                    60
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                               Query Match
Best Local S
Matches 20
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P25785;
01-MAY-1992
                                                                           DISULFID DISULFID DISULFID DISULFID CONFLICT CONFLICT CONFLICT CONFLICT CONFLICT
                                                                                                                                                                    DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 92290292.
SHIMIZU S., MALIK K., S
GENE 114:291-292(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1992 (REL.
01-APR-1993 (REL.
01-NOV-1995 (REL.
                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                     EMBL; M
                                                                                                                                                                                                                                                                                                          DISULFIDE BONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                   LECO K.J., HAYDEN L.J.,
EDWARDS D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-BA
                                                                                                                                                                                                                                                                                                                                  -!- PTM: THE ACTIVITY OF TIMP-2
                                                                                                                                                                                                                                                                                                                                                                                                                         GENE 117:209-217(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EUTHERIA; RODENTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rimp2 or rimp-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1992 (REL. 22, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
METALLOPROTEINASE INHIBITOR 2 PRECURSOR (TIMP-2)
                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 92347695.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METALLOPROTEINASES-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 KMHITICDFIVPWDTLSITQKKSLNHRYQMGCECKITRCPMIPCYISSPDECLWMDWVTE 180
                                                                                                                                                                                                                                                                                                                                           FUNCTION: COMPLEXES WITH METALLOPROTEINASES AND IRREVERSIBLY INACTIVATE THEM.
MGAAARSLRLALGLLLLASLVRPADACSCSPVHPQQAFCNADVVIRAKAVSEKEVDSGND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KSINGHQAKFFACIKRSDGSCAWYRGAAPPKQEFLDIEDP 220
                                                                                                                                                                                                                                        MGI:98753;
                                                                                                                                                                                                                                                               S15987; S15987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nmhitlcdfivpwdtlsatqkkslnhryqmgceckitrcpm1pcy1sspdec1
                                                                                                                                                                                                                                                                         X62622; G54802; -.
M82858; G202052; -.
M93954; G202054; -.
                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92290292.
                                                                                                                                                                                                                                                                                                                                                                            OGAWA K., YAMAMOTO S.,
                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                       TIMP2
                                                                                                                                                                                                                  INHIBITOR;
                                                                                                                                                                                                                                                                                                           HIGH WITH
                                                                                                                                                                                                                              TIMP;
                                           93.0%;
                                                                                       26
220
220
127
152
152
164
164
193
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                                                                            24328
                                                                                                                                                                                                                                                                                                                                                                                                  OF 27-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEJIMA H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                               SHARMA R.R., ROCHELEAU H.,
                                                                              MW;
                                                                                                                                                                                                                                                                                                           OTHER MEMBERS
                                                                                                                                                                                                                  SIGNAL.
                                                                                                                       METALLOPROTEINASE INHIBITOR 2
BY SIMILARITY.
                               Score 1536; DB 1;
Pred. No. 0.00e+00;
Pred. --+ches 7;
                                                                            L -> H (IN REF. 2)
V -> L (IN REF. 2)
K -> E (IN REF. 2)
W; EBC62FFC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                  IS DEPENDENT ON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KISHI J.I.,
                                                                                                                                                                                                                                                                                                                                                                              HAYAKAWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           220
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                                                                                                                                                                                                                                                                                                           THE TIMP FAMILY
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                                                                                       ้อออ
                                                      Length 220;
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                                                                                                                                                                                                                                                                                                                                                        (SUCH AS COLLAGENASES)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TISSUE INHIBITOR
                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               GREENBERG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KOIWAI O.;
                                  0;
                                  Gaps
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RESULT
ID T:
AC P:
AC P:
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                                                                                                                                                                                                                                                               MEDLINE; 95290091.
WILDE C.G., HAWKINS P.R., COLEMAN R.T.,
DELEGEANE A.M., OKAMOTO P.M., ITO L.Y.,
DNA CELL BIOL. 13:711-718(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 94215920.
SILBIGER S.M., JACOBSEN V.L.,
GENE 141:293-297(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIM3_HUMAN STANDARD; PRT; 211 AA. P35625; 01-JUN-1994 (REL. 29, CREATED) 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE) 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) METALLOPROTEINASE INHIBITOR 3 PRECURSOR (TIMP-3)
                                                                                                                                                                                                                         STOEHR H., I
GENOME RES.
                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE; 96404191.
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE; 95290091.
                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 94228524.
URIA J.A., FERRANDO A.A., VELAS
CANCER RES. 54:2091-2094(1994).
                                                   MEDLINE; 94245184.
APTE S.S., MATTEI M.-G.,
GENOMICS 19:86-90(1994).
                                                                                                                     SUBMITTED
                                                                                                                                                 SEQUENCE OF 42-211
                                                                                                                                                                     SUBMITTED (SEP-1996) TO EMBL/GENBANK/DDBJ DATA
                                                                                                                                                                                 TISSUE-RETINAL RUIZ A.C.;
                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE-BREAST CARCINOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-KIDNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HOMO SAPIENS (HUMAN)
EUKARYOTA; METAZOA; (
VARIANTS SED CYS-191 AND CYS-204.
MEDLINE; 95201800.
WEBER B.H.F., VOCT G., PRUETT R.C.,
NAT. GENET. 8:352-356(1994).
                                                                                                                                      TISSUE-PLACENTA
                                                                                                                                                                                                                                                                                                                                                              MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               METALLOPROTEINASES-3) (MIG-5 PROTEIN).
                                                                                              SEQUENCE OF 14-211
                                                                                                                                                                                                                                                                                                                                                    VICK M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EUTHERIA;
                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KMHITLCDFIVPWDTLSITQKKSLNHRYQMGCECKITRCPMIPCYISSPDECLMMDWVTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nmhitlcdfivpwdtlsatqkkslnhryqmgceckitrcpmipcyisspdeclwmdwvte 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FROM N.A.
94308155.
BUERGER C
                                                                                                                                                                                                                                                                                                                                          CHEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIMATES
                                                                                                                  (MAY-1996)
                                                                                                                                                                                                                        ROOMP K:, FELBOR U:, 5:483-487(1995).
                                                                                                                             HENRIET P.M.,
                                                                                                                                                                                          PIGMENT EPITHELIUM
                                                                                                                                                                                                                                                                                                                                        ER C., BRUESSELBACH S., 269:18953-18960(1994).
                                                                                              FROM N.A.
                                                                                                                                                FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHORDATA;
                                                                                                                 TO EMBL/GENBANK/DDBJ
                                                               OLSEN B.R.;
                                                                                                                             SILBIGER S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                     VELASCO G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CUPPLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERTEBRATA;
                                                                                                                                                                                                                                  WEBER B.H.F.;
          STOEHR H.,
                                                                                                                                                                                                                                                                                                                                                   LUCIBELLO
                                                                                                                                                                                                                                                                                                                                                                                                      FREIJE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R.L.,
                                                                                                                                                                                                                                                                                      SCOTT R
                                                                                                                          DECLERCK Y.A.;
                                                                                                                DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KOSKI R.A.;
                                                                                                                                                                                                                                                                                  R.W., SEILHAMER
                                                                                                                                                                                                                                                                                                                                                                                                    3
            FELBOR
                                                                                                                                                                     BANKS.
                                                                                                                                                                                                                                                                                                                                                  Ε.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TISSUE
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                                                                                                                                                                                                                                                                                                                                                   MUELLER
            ď.;
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Best Local S
Matches
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EMBL; U02571; G472310
EMBL; W02571; G495252
EMBL; X76227; G495252
EMBL; Z30183; G520932
EMBL; Z30183; G998826
EMBL; U33114; G121568
EMBL; U33111; G121568
EMBL; U33112; G121568
EMBL; U33112; G121568
EMBL; U33112; G121568
EMBL; U38955; G130448
EMBL; U38952; G130448
EMBL; U38953; G130448
EMBL; U38953; G130448
EMBL; U38954; G130448
EMBL; U38954; G130448
EMBL; U38954; G130448
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VARIANT SFD CYS-179.
MEDLINE; 96177683.
"CTOPHR H.
                                                                                                                                                                           CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                          VARIANT
VARIANT
                                                                                                                                                                                                                                                           DISULFID DISULFID
                                                                                                                                                                                                                                                                                  DISULFID DISULFID
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                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND IRREVERSIBLY INACTIVATE THEM. MAY FORM PART OF A TISSUE-
SPECIFIC ACUTE RESPONSE TO REMODELING STIMULI.

-!- SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX.

-!- DISEASE: DEFECTS IN TIME3 ARE THE CAUSE OF SORSBY'S FUNDUS

-!- DISEASE: DEFECTS IN THE SOURTH DECADE. IT IS CHARACTERIZED BY LOSS
DYSTROPHY (SFD), A RARE AUTOSOMAL DOMINANT MACULAR DISORDER WITH
AN AGE OF ONSET IN THE FOURTH DECADE. IT IS CHARACTERIZED BY LOSS
OF CEMTRAL VISION FROM SUBRETINAL MEDVASCULARIZATION AND ATROPHY
OF THE OCCULAR TISSUES. GENERALLY, MACULAR DISCIFORM DEGENERATION
DEVELOPS IN THE PATIENTS EYE WITHIN 6 MONTHS TO 6 YEARS.

-!- SIMILARITY: HIGH WITH OTHER MEMBERS OF THE TIMP FAMILY.
                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 96177683.
FELBOR U., STOEHR H., AMANN T., SCHOENHERR U., WEBER B.H.F.;
HUM. MOL. GENET. 4:2415-2416(1995).
                                                                                                                                                                                                                                                  VARIANT
                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FELBOR U., STOWEBER B.H.F.;
                                                                                                                                                                                                                                                                                                                                                         METALLOPROTEASE
                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                MIM; 136900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT SFD CYS-191.
MEDLINE; 96341630.
133 KGLNYRYHLGCNCKIKSCYYLPCFVTSKNECLWTDMLSNFGYPGYQSKHYACIRQKGGYC 192
                                                               83
                                              75
                      d-gdieflytapaaavcgvsldiggkkeyliagkaegngnmhitlcdfivpwdtlsatqk
                                            KMPHVQYIHTEASESLCGLKLEVN-KYQYLLTGRVY-DGKMYTGLCNFVERWDQLTLSQR 132
                                                                                                               41.2%;
Similarity 43.7%;
87; Conservet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENET. 33:233-236(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STOEHR H.,
                                                                                                                                                                 211 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                G1215682;
G1215682;
G1215682;
G1215682;
G1304484;
G1304484;
G1304484;
G1304484;
G1519558;
G407035;
                                                                                                                                                              TIMP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMANN T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOINED.
JOINED.
JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOINED.
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                                                                                                                                                                                                                                                                                                                                                                    ۲
                                                                                                                                                                  MW.
                                                                                                                                                           METALLOPROTEINASE INHIBITOR 3.
BY SIMILARITY.
BY G(IN SFD).
Y-> C (IN SFD).
Y-> C (IN SFD).
Y-> T (IN REF. 3).
DW-> T (IN REF. 3).
AE-> PR (IN REF. 8).
AE-> PR (IN REF. 3).
AE-> PR (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                         SIGNAL;
                                                                                                                 Score 681; DB 1; I
Pred. No. 4.35e-150;
51; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCHOENHERR
                                                                                                                                                                                                                                                                                                                                                        DISEASE MUTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           u.,
                                                                                                                 51;
                                                                                                                                         Length 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APFELSTEDT-SYLLA
                                                                                                                 Indels 10;
                                                                                                                 Gaps
                      141
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Best Local :
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DISULFID
SEQUENCE
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01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
01-CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
01-CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
METALLOPROTEINASE INHIBITOR 3 PRECURSOR (TIMP-3) (TISS
METALLOPROTEINASES-3) (21 KD PROTEIN OF EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STASKUS P.W., MASIARZ F.R., PALLANCK L.J., HAWKES S.P.;
J. BIOL. CHEM. 266:449-454(1991).
-I- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
AND IREEVERSIBLY INACTIVATE THEM. MAY FORM PART OF A TISSUE-
SPECIFIC ACUTE RESPONSE TO REMODELING STIMULI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GALLUS (CHICKEN).
EUKARYOTA; METAZOA; CHOI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 92381050.
PAVLOFF N., STASKUS P.W., KISHANANI N.S.,
J. BIOL. CHEM. 267:17321-17326(1992).
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TISSUE-EMBRYONIC FIBROBLAST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIMP3 OR IMP-3.
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  202
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                                           194 SWYRGWAPPDKTIINATDP 212
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hes. 89; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A39043; A39043.
A43429; A43429.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             awyrgaappkqefldiedp
                                                                                                                                                                                                                                                                                                       AEACTCVPIHPQDAFCNSDIVIRAKVVGKKLMKDGP--FGT-M-R--YTVKQMKMYRGFQ 75
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                                                                                                                                                                                    d-qdiefiytapaaavcgvsldiggkkeyliagkaegngnmhitlcdfivpwdtlsatgk
  awyrgaappkqefldiedp
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PS00288; T
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151
164
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6 193
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BY SIMILARITY.
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Pred. No. 8.22e-150;
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-I - FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES).

-I - FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES).

-I - FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES).

-I - FUNCTION: COMPLEXES OF A TISSUE-SPECIFIC ACUTE RESPONSE TO REMODELING STIMULI.
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
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01-NOV-1997 (REL.
01-NOV-1997 (REL.
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                                                                                                                                                                                                    01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
METALLOPROTEINASE INHIBITOR 3 PRECURSOR (TIMP-3)
                                                                                                                                                                                                                                                                                                          TIM3_MOUSE 
P39876;
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                                                                                                                           TIMP3 OR TIMP-3 OR SÚN.
MUS MUSCULUS (MOUSE).
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SEQUENCE FROM N.A. MEDLINE; 94179361.
                                                                           EUTHERIA;
                                                                                                EUKARYOTA;
                                                                                                                                                                              METALLOPROTEINASES-3
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hqakffacikrsdgscawyrgaappkqefidiedp 220
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Similarity 41.9%;
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35, LAST SEQUENCE UPDATE)
35, LAST ANNOTATION UPDATE)
INHIBITOR 3 PRECURSOR (TIMP-3) (TISSUE INHIBITOR
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                                                                                                   CHORDATA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 672; DB 1;
Pred. No. 1.33e-14
57; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               METALLOPROTEINASE I
BY SIMILARITY.
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                                                                                                   VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                   TETRAPODA;
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                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 95036582.
APTE S.S., HAYASHI K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LECO
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                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                      EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-129,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COLBURN N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUN Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OLSEN B.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CANCER RES.
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            133
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                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TE S.S., OLSEN B.R., MURPHY G.;
BIOL. CHEM. 270:14313-14318(1995).
- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BIOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CO K.J., KHOP
                                                                                                                                                                                                                                                                                                    1; L27424; G439882; -...; Z30970; E264421; -...; L19622; G438811; -...; U26437; G1167534; JOINED.
1; U26434; G1167534; JOINED.
1; U26435; G1167534; JOINED.
1; U26436; G1167534; JOINED.
1; U26436; G1167534; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                  INDUCTION: HIGHLY INDUCED BY PHORBOL ESTER (PMA), TRANSFORMING GROWTH FACTOR-BETA 1. ALSO INDUCED BY
                                                                                 AEACTCSPSHPQDAFCNSDIVIRAKVVGKKLVKEGP--FGT-L--V-YTIKQMKMYRGFS
         KGLNYRYHLGCNCKIKSCYYLPCFVTSKNECLWTDMLSNFGYPGYQSKHYACIRQKGGYC
                                                 KMPHVQYIHTEASESLCGLKLEVN-KYQYLLTGRVY-EGKMYTGLCNFVERWDHLTLSQR 132
                                                                     adacscspvhpqqafcnadivirakavnkkevdsgndiygnpikriqyeikqikmfkg-p
                             d-qdiefiytapaaavcgvsldiggkkeyliagkaegngnmhitlcdfivpwdtlsatqk
 HEGAMYER G., COLBURN N.H.; RES. 54:1139-1144(1994).
                                                                                                               Similarity 43.7% 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HEGAMYER G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'CHEM. 270:19312-19319(1995)
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                                                                                                                                                                                                                                                   INHIBITOR;
                                                                                                                          40.78;
43.78;
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                                                                                                                                                         24182 MW;
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 SIGNAL.
                                                                                                                                                                METALLOPROTEINASE INHIBITOR 3
BY SIMILARITY.
                                                                                                              Score 672; DB 1; I
Pred. No. 1.33e-147;
51; Mismatches 51;
                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                       CCB6E436 CRC32;
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Best Local
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P20414;
01-FEB-1991
01-FEB-1991
01-FEB-1996
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  BOS TAURUS EUKARYOTA;
                                          TIMP1.
                                                                                METALLOPROTEINASE
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SUBMITTED (MAY-1995)
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01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
METALLOPROTEINASE INHIBITOR 3 PRECURSOR (TIMP
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                                                                                                                                                                                                                                                                 202
                                                                                                                                                                                                                                                                                      193 SWYRGWAPPDKSISNATDP 211
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SIMILARITY: HIGH WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MITTED (MAY-1995) TO EMBL/GENBANK/DDBJ DATA BANKS. FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH & AND IRREVERSIBLY INACTIVATE THEM. MAY FORM PART OF SPECIFIC ACUTE RESPONSE TO REMODELING STIMULI.
                                                                                                                                                                                                                                                               awyrgaappkqefldiedp
                                                                                                                                                                                                                                                                                                                                                                                     KGLNYRYHLGCNCKIKSCYYLPCFVTSKKECLWTDMLSNFGYPGYQSKHYACIRQKGGYC
                                                                                                                                                                                                                                                                                                                                                                                                                             d-qdiefiytapaaavcgvsldiggkkeyliagkaegngnmhitlcdfivpwdtlsatqk
                                                                                                                                                                                                                                                                                                                                                                                                                                                    KMPHVQYIHTEASESLCGLKLEVN-KYQYLLTGRVY-EGKMYTGLCNFVERMDHLTLSQR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         adacscspvhpqqafcnadivirakavnkkevdsgndiygnpikriqyeikqikmfkg-p
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  (BOVINE).
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(REL.
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                                                                                                                                                                                   STANDARD;
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                                 17, CREATED)
17, LAST SEQUENCE UPDATE)
. 33, LAST ANNOTATION UPDATE)
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CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA
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BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 666; DB 1; I
Pred. No. 5.98e-146;
51; Mismatches 52;
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                                                                                                                                                                      TIM1_PAPCY P49061;
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MEDLINE; 94257757.
SATOH T., KOBAYASHI K.,
                                                                                                               01-FEB-1996
01-FEB-1996
                     PAPIO CYNOCEPHALUS
EUKARYOTA; METAZOA;
EUTHERIA; PRIMATES.
                                                                            TIMP1.
                                                                                               METALLOPROTEINASE
                                                                                                                                                      01-FEB-1996
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BIOCHEM. BIOPHYS. RES. (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PMASGILLLLWLTAPSRACTCVPPHPQTAFCNSDVVIRAKFVGTAEVNE-TALYQRYEIK 64
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50:835-844(1994).
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                                                                                          33, CREATED)
33, LAST SEQUENCE UPDATE)
33, LAST ANNOTATION UPDATE)
INHIBITOR 1 PRECURSOR (TIMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31.0%;
                                       (YELLOW BABOON)
CHORDATA; VERT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 512; DB 1;
Pred. No. 6.82e-104
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                                         VERTEBRATA;
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                                                                                              (TIMP-1).
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                                         TETRAPODA; MAMMALIA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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Best Local
SEQUENCE FROM N.A.
MEDLINE; 85240567.
GASSON J.C., GOLDE D.W., KJ
KAUFMAN R.J., WONG G.G., TE
ORR E.C., CLARK S.C.;
NATURE 315:768-771(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIM1_HUMAN S
P01033; Q14252;
21-JUL-1986 (REI
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21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
METALLOPROTEINASE INHIBITOR 1 PRECURSOR (TIMP-1) (ERYTHROID
POTENTIATING ACTIVITY) (EPA) (TISSUE INHIBITOR OF METALLOPROTEINASES)
(FIBROBLAST COLLAGENASE INHIBITOR) (COLLAGENASE INHIBITOR).
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AND IRREVERSIBLY INACTIVATE THEM.
-i- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON
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                                                                                                                                                MEDLINE; 86040463.
DOCHERTY A.J.P., LYONS A. HARRIS T.J.R., MURPHY G., NATURE 318:66-69(1985).
                                                                                                                                                                                                                                                                            HOMO SAPIENS (HUMAN)
EUKARYOTA; METAZOA; (
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
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TISSUE-AORTA;
                                                                                                                                                                                                             MEDLINE; 86040463.
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                                                                                                                                                                                                                                                                                                                                           TIMP1 OR TIMP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plafcllllgtllpradacscspvhpqqafcnadivirakavnkkevdsgndiygn-pik
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                                                                                                                                                                                                                                                                                                  CHORDATA;
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                                           KAUFMAN S.E.,
TEMPLE P.A., 1
                                                                                                                                                                     REYNOLDS
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METALLOPROTEINASE I
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POTENTIAL.
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Pred. No. 1.27e-103
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                                           LEARY A.C., BROWN E.L.,
                                                                                                                                                                                         WRIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ERYTHROCYTE MATURATION,
                                                                                                                                                                                                                                                                                                    TETRAPODA;
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                                                                                                                                                                                             STEPHENS
                                                                                                                                                                                                                                                                                                      MAMMALIA
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MUTAGENESIS.

MEDLINE; 93041700.

MEDLINE; 93041700.

O'SHEA M., WILLENBROCK F., WILLIAMSON R.A., COCKETT M.I.,

O'SHEA M., WILLENBROCK F., WILLIAMSON R.A., COCKETT M.I.,

EREEDMAN R.B., REYNOLDS J.J., DOCHERTY A.J.P., MURPHY G.;

BIOCHEMISTRY 31:10146-10152(1992).

1- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)

1- AND IRREVERSIBLY INACTIVATE THEM. ALSO MEDIATES ERYTHROPOIESIS IN

VITRO; BUT, UNLIKE IL-3, IT IS SPECIES-SPECIFIC, STIMULATING THE

GROWTH AND DIFFERENTIATION OF ONLY HUMAN AND MURINE ERYTHROID

PROGENITORS.
                                                                                               EMBL;
EMBL;
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TISSUE-SYNOVIAL FLUID;
MEDLINE; 92111776.
OSTHUES A., KNAUEPER V., OB
OFFERS LETT. 296:16-20(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WILLIAMSON R.A., MARTSON F.A.O., ANGAL S., I MORRIS H.R., CARNE A.F., SMITH B.J., HARRIS BIOCHEM. J. 268:267-274(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE; 94123576.
OPBROEK A., KENNEY M.C., BROWN D.;
CURR. EYE RES. 12:877-883(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE; 86205964.

CARMICHAEL D.F., SOMMER A., THOMPSON R.C., ANDER
WELGUS H.G., STRICKLIN G.P.;

PROC. NATL. ACAD. SCI. U.S.A. 83:2407-2411(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 42-207 FROM N.A.
MATSUDA T., KOHNO K., KUWANO M.;
SUMMITTED (JUL-1992) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFIDE BONDS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBMITTED (SEP-1995) TO EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-40 FROM N.A. HARDCASTLE A.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RAPP G., FREUDENSTEIN J., SCHEIT K.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 91025550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                          :- SIMILARITY: HIGH WITH OTHER MI
MBL; X03124; G37183; -.
MBL; M12670; G182483; -.
MBL; X02598; G31189; -.
MBL; M59906; G189382; -.
MBL; S68252; E119406; -.
MBL; D11139; G220125; -.
MBL; D11139; G220125; -.
MBL; L47361; G994731; -.
MBL; L47361; G994731; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IOTECHNOLOGY 5:595-598(1987)
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                                                                                                                                                                                                           DISULFIDE BONDS
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                      PS00288; TIMP; 1
                                                          A23534
A35826
                                               S20318
                                                                                   ZYHUEP
          METALLOPROTEASE INHIBITOR;
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S T.J.R.,
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RESULT 13

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CC EUWARYOTA; ME
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01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDAT
METALLOPROTEINASE INHIBITOR 1 PRECURSOR (TI
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE; 89214135.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORYCTOLAGUS CUNICULUS (RABBIT; EUKARYOTA; METAZOA; CHORDATA;
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                                                                                                                                                                                                                             PROSITE; PS00288;
                                                                                                                                                                                                                                                                                                               AND IRREVERSIBLY INACTIVATE -!- PTM: THE ACTIVITY OF TIMP-1
                                                                                                                                                                                                                                                                                                                                               J. BIOL. CHEM. 264:7092-7095(1989).
                                                                                                                                                                                                                                                                                                                                                                                                    HOROWITZ S., DAFNI N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EUTHERIA; LAGOMORPHA.
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                                                                                                                                                                                                                                                                                                DISULFIDE BONDS
                                                                                                                                                                                                                                           ; J04712; G165743; A33350; A33350.
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                             METALLOPROTEINASE I
BY SIMILARITY.
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OR (TIMP-1).
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CRC32;
                                                                                                                                                                                                           ERYTHROCYTE MATURATION
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMITH G.W., GOETE T.L., ANTHONY R.V., SMITH M.F.;
ENDOCRINOLOGY 134:344-352(1994).
-i- EUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
-AND IRREVERSIBLY INACTIVATE THEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (REL.
01-OCT-1996 (REL.
METALLOPROTEINASE
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P50122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 94102210.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 hqakffacikrsdgscaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 riqyelkqikmfkgpdqdiefiytapaaavcgvsldiggkke-yliagkaegngnmhitl 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: HIGH WITH OTHER MEMBERS L; S67450; G456990; -. SITE; PS00288; TIMP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTM: THE ACTIVITY OF TIMP-1 DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CSFVVPWNSLSFSQRSGFTKTYAAGCDMCTVFACASIPCHLESDTHCLWTDSSLGSD-KG
                                                                                                                                                    LLLL-WLTAPSRACTCVPPHPQTAFCNSEVVIRAKFVGTAEVNE-TALYQRYEIKMTK-M 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTK-MFKGFDAL-GHATDIRFVYTPAMESVCGYSHKSQNRSEEFLIAGQLR-NGLLHITT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALASSMLLLLWLVAPSRACTCVPPHPQTAFCNSDLVIRAKFYGAPEVNHTT-LYQRYEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cdfivpwdtlsatqkkslnhryqmgce-ckitrcpmipcyisspdeclwmdwvtekning
PWNSMSSAQRRGFTKTYAAGCEECTVFPCSSIPCKLQSDTHCLWTDQLLTGSDKGFQSRH 186
                                                                FKGFSALRDA-PDIRFIYTPAMESVCGYFHRSQNRSEEFLIAGQL-SNGHLHITTCSFVA 126
                                                                                                                           llllgtllpradacscspvhpggafcnadivirakavnkkevdsgndiygn-pikrigye 72
                                          ikqikmfkgpdqdiefiytapaaavcgvsldiggkke-yliagkaegngnmhitlcdfiv
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79; Conser
                                                                                                                                                                                                                                   Similarity
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METAZOA; CHORDATA; VERTEBRATA;
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llarity 39.9%;
Conservative
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23057
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34, LAST SEQUENCE UPDATE)
34, LAST ANNOTATION UPDATE)
INHIBITOR 1 PRECURSOR (TIMP-1).
                                                                                                                                                                                                                                 30.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                203
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                                                                                                                                                                                                         Score 508; DB 1;
Pred. No. 8.19e-10:
42; Mismatches 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 508; DB 1; I
Pred. No. 8.19e-103;
38; Mismatches 73:
                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.

METALLOPROTEINASE I
BY SIMILARITY.
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890A6EEB CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73;
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                                                                                                                                                                                                                                                     Length 207;
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01-MAY-1991 (REL. 18, LAST SEQUENCE UPDATE)
01-MAY-1991 (REL. 35, LAST ANNOTATION UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
METALLOPROTEINASE INHIBITOR 1 PRECURSOR (TIMP-1) (ERYTHROID
POTENTIATING ACTIVITY) (EPA) (TISSUE INHIBITOR OF METALLOPROTEINASES)
(COLLAGENASE INHIBITOR 16C8 FIBROBLAST) (TPA-INDUCED PROTEIN)
         CHAIN
DISULFID
DISULFID
                                                                                                                                                                    EMBL;
                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                          JOHNSON M.D., HOUSEY G.M., KIRSCHMEIER P.T., WEINSTEIN I.B.;
MOL. CELL. BIOL. 7:2821-2829(1987).

-i- FUNCTION: COMPLEXES WITH METHALLOPROTEINASES (SUCH AS COLLAGENASES).

-AND IRREVERSIBLY INACTIVATE THEM. ALSO MEDIATES ERYTHROPOLESIS IN VITRO; BUT, UNLIKE IL-3, IT IS SPECIES-SPECIFIC, STIMULATING THE GROWTH AND DIFFERENTIATION OF ONLY HUMAN AND MURINE ERYTHROID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBO J. 6:651-657(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MUS MUSCULUS (MOUSE
EUKARYOTA; METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIM1_MOUSE
                                                                                                                                                                                                                             EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P12032; P20064
                                                       SIGNAL.
                                                                                                                                                EMBL;
                                                                                                                                                            EMBL;
                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                        DISULFIDE B
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EDWARDS D.R.,
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                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 88038821.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEIC ACIDS
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132 pwdtlsatqkksinhryqmgce-ckitrcpmipcyisspdeclwmdwvtekninghqakf 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187 LACLPREPGMCTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     191 facikrsdgscaw
                                                                            LYCOPROTEIN;
                                                                                                                                                                                                                                                                                              TISSUE SPECIFICITY: FOUND IN FETAL AND ADULT TISSUES. HIGHEST LEVELS ARE FOUND IN BONE. ALSO FOUND IN LUNG, OVARY AND UTERUINDUCTION: BY VIRUS.
                                                                                                                                                                                                                                                                                    INDUCTION: REGULATED BY TUMOR PROMOTERS AND
                                                                                                                                                                                                                                                                         PROTEIN KINASE C
                                                                                                                                                                    M28311; G193042;
X04684; G49704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OR TIMP-1
                                                                                                                                                                                                                 M28312; G193042;
M28308; G193042;
                                                                                                                                                                                                                                                  SULFIDE BONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87066763
                                                                                                                                                                                                                                                            THE ACTIVITY OF TIMP-1
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                                                                                                                                                                             G193042; JOINED.; G193042; JOINED.; G193042; JOINED.; G193042; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MOUSE)
 1
25
25
27
27
151
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                                                                              METALLOPROTEASE INHIBITOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OR TIMP.
                                                                                                                                                                                                                                        HIGH WITH OTHER
                                                                                         TIMP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            199
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 24
205
94
123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В.,
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METALLOPROTEINASE I
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                        MEMBERS OF
                                                                                                                                                                                                                                                               IS DEPENDENT ON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205
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                                                                               ERYTHROCYTE MATURATION;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DENHARDT
                                                                                                                                                                                                                                        THE TIMP FAMILY
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                                              INHIBITOR
                                                                                                                                                                                                                                                               THE
                                                                                                                                                                                                                                                                                     MITOGENS THROUGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WILLIAMS B.R.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U
                                                                                                                                                                                                                                                               PRESENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAMMALIA;
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(ME)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

: 40 C bular output not generated. Mon May 4 14:47:31 1998; MasPar time 17.84 Seconds 519.169 Million cell updates/sec

Title:

Description: Perfect Score: Sequence:

>R07954 (1-220) from a-geneseq.pep 1651 1 mgaaarslplafc1lllgt1.....cawyrgaappkqefldiedp 220

Scoring table: PAM 150 Gap 11

Searched: 140555 seqs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

sptremb15

Database:

1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal 5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant 9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate 13:sp_unclassified

Statistics: Mean 43.195; Variance 65.893; scale 0.656

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match L	Length	80	ID .	Description	Pred. No.
1	1430	86.6	196	10	Q60453	CISSUE INHIBITOR OF ME	0.00e+00
N	1285	77.8	220	12	042146		0.00e+00
w	817	49.5	224	N	Q99727	TISSUE INHIBITOR OF ME	4.20e-182
4	460	27.9	207	4	002722	TISSUE INHIBITOR OF ME	2.90e-87
U	. 455		176	10	P70533	METALLOPROTEINASE INHI	5.72e-86
o,	249	15.1	50	N	Q16121	TIMP-2-METALLOPROTEINA	1.95e-34
7	213	12.9	158	ω	Q21265	SIMILAR TO METALLOPROT	5.02e-26
80	99		38	10	Q61720	MESSENGER RNA FRAGMENT	1.60e-02
9	92	5.6	512	æ	Q40271	MYO-INOSITOL-1-PHOSPHA	2.23e-01
10	92	5.6	668	9	Q48297	HISTIDINE KINASE.	2.23e-01
11	91	5.5	376	80	Q39353	CELL WALL-PLASMA MEMBR	3.21e-01
12	. 89	5.4	113	10	Q61259	ABELSON MURINE LEUKEMI	6.61e-01
13	89	5.4	114	10	Q61260	ABELSON MURINE LEUKEMI	6.61e-01
. 14	89	5.4	115	ν	Q13691	ABL PROTEIN (FRAGMENT)	6.61e-01
15	89	5.4	119	10	P97896	ABELSON MURINE LEUKEMI	6.61e-01
16	89	5.4	119	ν	Q13915	C-ABL (FRAGMENT).	6.61e-01
17	89	5.4	138	10	Q61261	ABELSON MURINE LEUKEMI	6.61e-01
18	89	5.4	144	N	Q13848	BCR/C-ABL ONCOGENE PRO	6.61e-01
19	89	5.4	156	N	Q14020	BCR/C-ABL ONCOGENE PRO	6.61e-01
20	89	5.4	164	2	Q13690	HYPOTHETICAL PROTEIN (6.61e-01

45	44	4 3	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	
85	8 5	84	<u>8</u> 5	86	86	86	86	86	86	86	88	88	87	87	88	68	89	89	89	89	89	89	89	89	
5.1			٠		5.2	5.2	5.2	5.2	5.2	5.2	5.3	5 .3	5.3	ω	ح. س	5.4	5.4	٥. 4.	5.4	5.4	5.4	5.4	5.4	5.4	
1014	589	506	249		1010	1010	988	987	323	231	1117	476	383				1130	583	433	284		187	182	181	
10	ω	9	ω	11	N	N	N	N	N	ω	ø	_	10	7	11	N	N	9	ω	N	10	5	0	5	
035937	Q17935	P96824	Q20700	041943	015330	000754	Q93094	Q16680	Q93093	Q19567	Q53971	Q12619	Q62779	Q37993	041968	Q13869	Q13870	030411	Q23275	Q13692	Q61252	Q61254	061255	Q61253	
POLY(ADP-RIBOSE) POLYM :	C12D8.1A.	HYPOTHETICAL 55.0 KD P	COSMID F53B1.	MAJOR CAPSID PROTEIN. :	LYSOSOMAL ALPHA-MANNOS :	ALPHA-MANNOS	LYSOSOMAL ACID ALPHA-M :	ALPHA-MANNOSIDASE (EC :	TRUNCATED LYSOSOMAL AC :	COSMID F18E9.	FIBRONECTIN BINDING PR !	ACYL-COA DESATURASE 1 9	PREADIPOCYTE FACTOR 1.	MAJOR HEAD PROTEIN.	TEGUMENT PROTEIN.		PROTO-ONCOGENE TYROSIN (PUTATIVE ABC-TRANSPORT (SIMILAR TO S. CEREVISI (BCR/ABL FUSION PROTEIN	C-ABL PROTEIN, TYPE IV	н	C-ABL PROTEIN, TYPE II (C-ABL PROTEIN, TYPE II	
2.69e+00	2.69e+00	3.79e+00	2.69e+00	1.90e+00	1.90e+00	1.90e+00	1.90e+00	1.90e+00	1.90e+00	1.90e+00	9.44e-01	9.44e-01	1.34e+00	1.34e+00	9.44e-01	6.61e-01	6.61e-01	6.61e-01	6.61e-01	6.61e-01	6.61e-01	6.61e-01	6.61e-01	6.61e-01	
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ALIGNMENTS

	Qy Qy	ļ	Qy V
Query Match 86.6%; Score 1430; DB 10; Length 196; Best Local Similarity 94.4%; Pred. No. 0.00e+00; Matches 184; Conservative 9; Mismatches 2; Indels 0; Gaps 0	TEETVE DOCUMENT TO COMPANY TO A PROPERTY TO A PROPERTY TO A PROPERTY OF THE TWO WITH THE PROPERTY OF T		
		62 IEFIYTAPSSAYCGYSLDYGGKKEYLIAGKAEGDGKMHITLCDFIYPWDTLSTTQKKSLN :: :	62 IEFIYTAPSSAYCGYSLDYGGKKEYLIAGKAEGDGKMHITLCDFIVPWDTLSTTQKKSLN

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01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCI
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTAT
01-YAN-1998 (TREMBLREL. 05, LAST ANNOTAT
                                                                                                                                                                                          099727;
01-MAY-1997 (TREMBLREL. 03, CREATED)
01-MAY-1997 (TREMBLEEL. 03, LAST SEQUENCE UPDATE)
01-MAY-1997 (TREMBLEEL. 03, LAST ANNOTATION UPDATITISSUE INHIBITOR OF METALLOPROTEINASE 4.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METALOA; CHORDATA; VERTEBRATA; TETRAPOLEUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                     LT 3
Q99727
                                                                                                                               GREENE J., WANG M., RAYMOND L.A., LIU Y.E., ROSUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA EMBL; U76456; G1773293; -.
                                                                                                                                                             TISSUE-HEART;
                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

AIMES R.T., LI L., WEAVER B., HAWKES S., F
SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ
EMBL; AF004664; G2352473; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GALLUS GALLUS (CHICKEN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                     KMHITLCDLVATWDSVSPTQKKSLNQRYQMGCECKISRCLSIPCFVSSSDECLWTDWAME
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         ASADP-ADTEKMLRYEIKQIKMFKGFEKVKDVQYITTPFDSSLCGVKLEANSQKQYLLTG 118
                                                                                                                                                                                                                                                                                                                                               KIVGGRQAKHYACIKRSDGSCAWYRGMAPPKQEFLDIEDP 220
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                                                                                102;
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170; Conse
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                                                                                                                       224 AA;
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                                                                                Conservative
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220 TI
24313 MW;
                                                                                        49.5%;
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77.3%;
                                                                                                                      25502 MW;
                                                                              Score 817; DB 2; Le
Pred. No. 4.20e-182;
59; Mismatches 57;
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25; 1
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 0.00e+00;
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TISSUE INHIBITOR OF
; F477B394 CRC32;
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                                                                                                                                                                                                     TETRAPODA;
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                                                                                                                                          ROSEN C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
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Best Local
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                     TISSUE-LIVER:
IREDALE J.P., BENYON R.C., ARTHU
WINWOOD P.J., CLARK N., MURPHY G
HEPATOLOGY 24:176-184(1996).
EMBL; L29512; G1550734; -.
NON_TER 1 1
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002722
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                                                                                                                                                                                                                                                                                 01-FEB-1997 (TREMBLREL.
01-FEB-1997 (TREMBLREL.
01-FEB-1997 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQUUS CABALLUS (HORSE).
EUKARYOTA; METAZOA; CHORDATA;
EUTHERIA; PERISSODACTYLA.
    SEQUENCE
                                                                                                                                                                                                   RATTUS NORVEGICUS (
EUKARYOTA; METAZOA;
                                                                                                                                                                                                                                             TIMP-1
                                                                                                                                                                                                                                                                                                                                              P70533
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                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                EUTHERIA;
                                                                                                                                                                                                                                                              METALLOPROTEINASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIMP-1
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01-JUL-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 ninghqakffacikrsdgscaw
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(TREMBLREL.
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  AA;
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  19659 MW;
                                                                                                                                                                                                     CHORDATA;
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05,
                                                                             ARTHUR RPHY G.;
                                                                                                                                                                                                                                                                             CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         199
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Pred. No. 2.
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                                                                                                                                                                                                     VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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  7CB8A5D1
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                                                                                                M.J.,
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.90e-87;
CRC32;
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                                                                                                                                                                                                                                                                                 UPDATE)
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               BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A GRANTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L., GARDNER A., GRÈEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P., LIGHTNING J., LLOYD C., MCMUTRAY A., MORTIMORE B., O'CALLAGHAN M., PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN M., WATERSTON R.,
                                                                                                                                                                                                                                                                                                        LT 7
Q21265
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Q16121
                                                                                                                                                                                                                                                                   Q21265;
01-NOV-1996
          THIERRY-MIEG J., THOMAS K., WATSON A., WEINSTOCK L., WI
                                                                                                                                    STRAIN-BRISTOL N2;
MEDLINE; 94150718.
                                                                                                                                                                                        CAENORHABDITIS ELEGIEUKARYOTA; METAZOA;
                                                                                                                                                                                                                               SIMILAR TO METALLOPROTEINASE
                                                                                                                                                                                                                                           01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DE CLERCK Y.A., DARVILLE M.I.,
GENE 139:185-191(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUKARYOTA; METAZOA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q16121;
                                                                                                          WILSON R., AINSCOUGH R., BONFIELD J., BURTON J.,
                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HOMO SAPIENS (HUMAN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIMP-2=METALLOPROTEINASE-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117
                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity les 35; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92
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                                                                                                                                                                                                                                                                                                                                                                         1 MGAAARTLRLALGLLLLATLLRPADACSCSPVHPQQAFCNADV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ш
                                                                                                                                                                                                                                                                                                                                                          mgaaarslplafcllllgtllpradacscspvhpqqafcnadi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCGVCTVFPCSVIPCKLESDTHCLWTDQILMGSEKGYQSRHLACLPRNPGLCTW 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAMESICGYVHKSQNRREEFILIAGRIR-NGNIHITACSFIVPWASISPAQRKGITKTYSA 116 :: ::|| | : || :| :| :| :| |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gce-ckltrcpm1pcy1sspdeclwmdwvtekninghqakffacikrsdgscaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              apaaavcg-vsldiggkkeyliagkaegngnmhitlcdfivpwdtlsatgkkslnhryqm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HPQTAFCNSDLVIRAKFMGSPEI-IETTLYQRYEIKMTK-MLKGFDAV-GNATDIRFAYT 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hpqqafcnadivirakavnkkevdsgndiygn-pikriqyeikqikmfkgpdqdiefiyt 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS00288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94156197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               50 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       191(12);
; E119468; -.
TMP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50
                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                       ELEGANS.
AZOA; ACOELOMATES;
                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                5121 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                          15.1%;
81.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHORDATA;
                                                                                                                                                                                                                                         01,01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30,0
           WILKINSON-SPROAT
                                                                                                           ANDERSON K., BAYNES C., BERKS M.
CONNELL M., COPSEY T., COOPER J.,
                                                                                                                                                                                                                                                                                                                                                                                                             Score
Pred.
4; M
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LAST SEQUENCE UPDATE)

LAST ANNOTATION UPDATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. 34; 1
                                                                                                                                                                                                                            LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
E INHIBITOR 2 PRECURSORS
                                                                                                                                                                                                                                                                    CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                4992D252 CRC32;
                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EECKHOUT
                                                                                                                                                                                        NEMATODA;
                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                           249; DB 2;
No. 1.95e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INHIBITOR { PROMOTER
                                                                                                                                                                                                                                                                                                          158
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atches 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50
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                                                                                                                                                                                                                               PRECURSORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TETRAPODA;
                                                                                                                                                                                        SECERNENTEA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ROUSSEAU
                                                                                                                                                                                                                                                                                                                                                                                                              4
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                            43
                                                                                                                                                                                                                                                                                                                                                                                     43
                                                                                                                       BERKS M.,
                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                       50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (FRAGMENT)
                                                                                   JOHNSTON L.,
                                                                                                                                                                                        RHABDITIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
                                                                                                                                                                                                                                                                                                                                                                                                              0,
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RESULT
ID Q4
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SO REAL REPORTS
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Best Local Similarity
Matches 37; Conser
                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [2]
SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
WU X, LE TT.;
                                                                                                                                                                                                                                                         EUKUHARA H., DE MAEYER-GUIGNARD J., DE WICLEIC ACIDS RES. 10:3069-3084(1982).
EMBL; V00755; G817965; -.
EMBL; J00425; G194118: -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  261720
                               01-NOV-1996 (TREMBLREL. 01, 01-NOV-1996 (TREMBLREL. 01, 01-JAN-1998 (TREMBLREL. 05, 01-JAN-1998) (TREMBLREL. 05, MYO-INOSITOL-1-PHOSPHATE SYN
                                                                            Q40271;
                                                                                                   Q40271
                                                                                                                                                                                                                                                                                                                                                                                     THE C-TERMINAL PART MUS MUSCULUS (MOUSE)
                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-FEB-1997 (TREMBLREL. 02, LAST ANNOTATION UPDAT
MESSENGER RNA FRAGMENT FOR MOUSE INTERFERON BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q61720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBMITTED (APR-1996) TO EMBL; U53336; G1255824;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
CARYOPHYLLALES;
                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WATERSTON R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBMITTED
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE; 82247191.
                                                                                                                                                                                                                                                                                                                                                                 EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TREMBLREL.
                   MESEMBRYANTHEMUM CRYSTALLINUM (COMMON
                                                                                                                                                  172
                                                                                                                                                                                                                                                                                                                                                                             EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 itlcdfivp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 TVLCGQVLP 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10
                                                                                                                                                               2 CLWTDQVLVGS-EDYQSRHFACLPRNLGLCTW 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 LSLSLVILSVLIAVTLACKCREQSTKESFCNAHWVSHVKVKVRVGKQGLPEGSERKG--L
                                                                                                                                               clwmdwvtekninghqakffacikrsdgscaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            kriqyeikqikmfkgp-dqd-i-eflytapaaavcgvsldiggkkeyllagkaegngnmh 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NNLRYTVOHVEVFKKPSNMTTLPDEIFTPSEAPACG--LKIAAGHEYLLAGRVEGPNALY 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lafcllllgtllpradacscspvhpqqafcnad-iv-iraka-vnkkevdsgndiygnpi
                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (APR-1996)
                                                                                                                                                                                                                                                                                                                                                                          METAZOA; CHORDATA; VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      158 AA;
                                                                                                                                                                                                                                             38 AA; 4390 MW;
                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <del>..</del>
                                                                                                  PRELIMINARY;
                                                                                                                                                                                                          6.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17465 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                         LAST SEQ
                                                                                                                                                                                            Score 99;
Pred. No.
7; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 213; DB 3;
Pred. No. 5.02e-26;
38; Mismatches 44
                                        LAST SEQUENCE UP
                                                                 CREATED)
                                                                                                                                                                                                                                              429816C2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FBD8E38D CRC32;
         ANGIOSPERMAE;
                                                                                                                                                                                                                                                                                                      GEORGE H., W
                                                      SEQUENCE UPDATE;
                                                                                                                                                                                                Mismatches
                                                                                                   512
                                                                                                                                                                                               1.60e-02;
atches 11;
                    ICE PLANT)
                                                                                                                                                  203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38
                                                                                                                                                                                                                       DB 10;
                                                                                                   B
                                                                                                                                                                                                                                                                                                                                                                             TETRAPODA; MAMMALIA;
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                                                                                                                                                                                                                                                                                                       WILLIAMS
                                                                                                                                                                                                                                                                                                                                                                                                              UPDATE)
BETA (TYPE
                                         UPDATE)
          DICOTYLEDONEAE;
                                                                                                                                                                                                                      Length
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                                              Query Match
Best Local S
Matches 1
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Best Local Similarity 38.9%;
Matches 14; Conservative
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE; 96208959.

ISHITANI M., WAJUMDER A.L., B
JENSEN R.G., BOHNERT H.J.;

PLANT J. 9:537-548(1996).

EMBL; U32511; G975888; -.

SEQUENCE 512 AA; 56758 MW;
                                                                                                                                                                                                                                    Q39353;
01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q48297;
01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
                                                                                      STRAIN-CV. COBRA;
GOODMIN W.G., PALLAS J.A., JENKINS G.I.;
SUBMITTED (JAN-1996) TO EMBL/GENBANK/DDBJ DATA
EMBL; X94976; E218269; -.
SEQUENCE 376 AA; 38667 MW; FD5D37DD CRC32;
                                                                                                                                                                                                                                                                                                 LT 11
Q39353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LT 10
Q48297
                                                                                                                                                                                                                     01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
CELL WALL-PLASMA MEMBRANE LINKER PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                          RUDOLPH J., OESTERHELT D.;
EMBO J. 14:667-673(1995).
EMBL; X82645; G671100; -
SEQUENCE 668 AA; 71931 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE; 95188871.
                                                                                                                                                                                      BRASSICA NAPUS (RAPE).
EUKARYOTA; PLANTA; EMBRYOPHYTA;
                                                                                                                                                                               CAPPARALES; CRUCIFERAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARCHAEBACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HALOBACTERIUM SALINARIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HISTIDINE KINASE.
                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                     549 VESGGEEYGIPIKTVD-EISRMKSVKSVDGEEVITY 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          275 EENIPFINGSPONTFVPGL-IDLAIKKNSLIGGDDFKSGQTKMKSVLVDFLV 325
                                                                                                                                                                                                                                                                                                                                                55
                                              Match 5.5%;
Local Similarity 44.1%;
les 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mgaaarslplafcllllgtllpradacscspvhp
            MGSHTQNLSFLI-LLLLG-FLAVSFACECSPPKP 32
                                                                                                                                                                                                                                                                                                                                               vdsgndiygnpikriqyeikqikmfkgpdqdiefiy 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 5.6%;
Similarity 34.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EURYARCHAEOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56758 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22,0
                                             Score 91; D
Pred. No. 3.
10; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                           Score 92; D
Pred. No. 2.
9; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 92; D
Pred. No. 2.
13; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BORNHOUSER A., MICHALOWSKI C.B.,
                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HALOBACTERIALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                           3D4B7F92 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8F97FE26 CRC32;
                                                                                                                                                                                       ANGIOSPERMAE;
                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   899
                                                         DB 8; I
3.21e-01;
                                                                                                                                                                                                                                                                                                                                                                                                       DB 9; I
2.23e-01;
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2.23e-01;
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                                                                     Length 376
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ID Q61259
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                                                                                                                                                                                                                                                                                       Query Match 5.4%;
Best Local Similarity 42.1%;
Matches 16; Conservative
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Best Local Similarity 42.1%;
Matches 16; Conservative
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MEDLINE; 86133550.

BEN-NERTAH Y, BERNARDS A., F
CELL 44:577-586(1986).

EMBL; M12263; G191561; -...
              Q13691;
01-NOV-1996
01-NOV-1996
01-NOV-1996
ABL PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q61260;
01-NOV-1996
01-NOV-1996
01-JAN-1998
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Q13691
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01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LT 13
Q61260
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NON_TER
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NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUS MUSCULUS (MOUSE)
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EUTHERIA; RODENTIA.
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|| |:|| :| :| ::| ||: : | ||| |
108 keyllagkaegngnmhitlcdfivpwd-tlsatqkksl 144
                                                                                                                                                                                                                                46 KENLLAGPSENDPNLFVALYDFVASGDNTLSITKGEKL 83
                                                                                                                                                                                                                                                                                                                                                                                      MGI:87859; ABL.
TER 114 114
                                                                                                                                                                                                                                                                                                                                                                                                                           NERIAH Y., BERNARDS
44:577-586(1986).
; M12264; G191563;
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TER 113 1
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                              (TREMBLREL.
(TREMBLREL.
(TREMBLREL.
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(TREMBLREL.)
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12519 MW;
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01, LAST
05, LAST
000COGENE
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01, LAST SEQUENCE UPDATE)
05, LAST ANNOTATION UPDATE)
0NCOGENE (C-ABL TYPE II MRNA)
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Pred. No. 6.61e-0
8; Mismatches
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Pred. No.
8; Misma
                              CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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6.61e-01;
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Page 5
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Search completed: Mon May 4 14:47:55 1998 Job time: 24 secs.
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ID P97896
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                                                                                                                                          Query Match 5.4%;
Best Local Similarity 42.1%;
Matches 16; Conservative
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Best Local Similarity 42.1%;
Matches 16; Conservative
                                                                                                                                                                                                             MGD: MGI:87859; ABL.
NON_TER 119 119
SEQUENCE 119 AA; 13013 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABL.
MUS MUSCULUS (NOUSE).
MUS MUSCULUS (NOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1997 (TREMBLREL.
01-MAY-1997 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE; 85240529.

SHITVELMAN E., LITSHITZ B., GALE R.P., CANAANI E.;

NATURE 315:550-554(1985).

EMBL; M30833; G553164; -.

NON_TER 115 115

SEQUENCE 115 AA; 12628 MW; A9E82733 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                               51 KENLLAGPSENDPNLFVALYDFVASGDNTLSITKGEKL 88
|| |:|| :| :| :| ||: :| ||| ||
108 keyliagkaegngnmhitlcdfivpwd-tlsatqkksl 144
                                                                                                                                                                                                                                                                                                                           NCOGENE 2:297-304(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                  EDLINE; 86133550.
EN-NERIAH Y., BERNARDS A., PASKIND M., DALEY G.Q., BALTIMORE D.;
ELL 44:577-586(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BELSON MURINE LEUKEMIA
                                                                                                                                                                                                                                                                 MBL; K03228; G191559; -. MBL; K07539; G49838; -. MBL; M12265; G53852; -.
                                                                                                                                                                                                                                                                                                                                                            EQUENCE OF 1-26 FROM N.A. IRAIN-BALB/C; TISSUE-LIVER; 88202920.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 KENLLAGPSENDPNLFVALYDFVASGDNTLSITKGEKL 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                          PASKIND M., BALTIMORE D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03, CREATED)
03, LAST SEQUENCE UPDATE)
05, LAST ANNOTATION UPDATE)
0NCOGENE (C-ABL PROTEIN) (FRAGMENT).
                                                                                                                                        Score 89; DB 10;
Pred. No. 6.61e-01;
8; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 89; DB 2; Length 115;
Pred. No. 6.61e-01;
8; Mismatches 13; Indels
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                                                                                                                                                                                                                 92DAB735 CRC32;
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Jular output not generated. on: Mon May 4 14:51:51 1998; MasPar time 9.10 Seconds 361.220 Million cell updates/sec

Scoring table: Sequence: Description: Perfect Score: Title: >R07955 (1-220) from a-geneseq.pep 1643 PAM 150 Gap 11 1 mgaaartlrlalgllllatl.....cawyrgaappkqefldiedp 220

Searched: 120837 seqs, 14945562 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq31 i:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26

Statistics: Mean 32.207; Variance 121.307; scale 0.265

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Length	BG	ID	Description	Pred. No.
р:	1643	100.0	220	13	R65009	Human tissue inhibito	2.41e-169
N	1643	100.0	220	12	R62769	Human metalloproteina	2.41e-169
w	1643	100.0	220	N	R07955	Human metalloproteina	2.41e-169
4	1550	94.3	220	12	R62768	Bovine metallopTotein	8.23e-159
u	1550	94.3	220	N	R07954	Bovine metalloprotein	8.23e-159
6	1454	88.5	194	N	R06898	Complete sequence of	5.97e-148
7	1396	85.0	186	N	R06896	Part of TIMP-2 metall	2.14e-141
8	1377	83.8	192	N	R06895	Metalloproteinase inh	2.99e-139
9	1337	81.4	177	N	R06897	Part of TIMP-2 metall	9.82e-135
10	844	51.4	224	23	W25603	Tissue inhibitor of m	2.16e-79
11	842		224	18	R98265	Tissue inhibitor of m	3.61e-79
12	718	43.7	211	25	W30310	Human TIMP-1/TIMP-3 f	2.16e-65
13	695	42.3	211	15	R84215	TIMP-3 clone-7 produc	7.60e-63
14	695	42.3	211	13	R72598	TIMP-3 metalloprotein	7.60e-63
15	687	41.8	206	13	R65014	Human tissue inhibito	5.83e-62
16	686	41.8	212	13	R65002	Chicken tissue inhibi	7.52e-62
17	685	41.7	198	15	R84216	TIMP-3 clone-2 produc	9.70e-62
. 18	683	41.6	211	13	R65001	Mouse tissue inhibito	1.61e-61
19	672	40.9	188	25	W30308	Human TIMP-3.	2.65e-60

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61 iygnpikriqyeikqikmfkgpekdiefiytapssavcgvsldvggkkeyliagkaegdg 120

Query Match 100.0%; Best Local Similarity 100.0%; Matches 220; Conservative

Score 1643; DB 13; Length 220; Pred. No. 2.41e-169; 0; Mismatches 0; Indels 0;

Indels 0;

Gaps

0;

44	42 43	41	40 40	38	. 37	36	ა 5	34	33	32	31	30.	29	28	27	26	25	24	23	22	21	20
128 118	131 130	137	140 139	147	149	157	170	219	323	475	481	503	506	.516	517	521	521	521	521	523	556	637
7.8	7.9	8.3	æ œ ∵ ∵	8.9	9.1	9.6	10.3	13.3	19.7	28.9	29:3	30.6	30.8	31.4	31.5	31.7	31.7	31.7	31.7	31.8	33.8	38.8
15 20 6			ωα										205 13	207 3	207 13		207 3		207 3		164 19	184 13
	R65011 R06748		R06747							R65008			R65007	P60593	R65003	W30309		P60275	P60592	R65006	R84217	R65000
ro 6	Tissue inhibitor of m 3.35e-03 Immunogenic TIMP-2 pe 4.13e-03	digestion pro 9.44e	Peptide #2 for detect 6.17e-04	sequence o 1	e o 7	teinase inh 1	tect 7.20e-	proteinase inh 1.05e-	or detect 1.92e-	e tissue inhibito 1	Pig tissue inhibitor 2.28e-39	Human tissue inhibito 9.25e-42	inhibito 4	Sequence of a gibbon 3.55e-43	Cattle tissue inhibit 2.76e-43	l. 1.01e-	of tissue in 1.01e-	human na	Sequence of a human p 1.01e-43	Rabbit tissue inhibit 6.12e-44	1.52e-	Chicken inhibitor of 1.92e-56

ALIGNMENTS

RESULT	IT 1 R65009 standard: Protein: 220 AA.
AC.	R65009;
ď	24-OCT-1995 (first entry)
Œ	Human tissue inhibitor of metalloproteinase (TIMP-2).
ΚW	Tissue inhibitor of metalloproteinase; diagnostic; therapeutic;
WW	prophylaxis.
လ	Homo sapiens.
PN	WO9505478-A.
•	23-FEB-1995.
	12-AUG-1994; U09188.
PR	12-AUG-1993; US-105263.
	13-DEC-1993; US-167463.
PA	(REGC) UNIV CALIFORNIA.
ΡI	Hawkes SP, Kishnani NS, Yang T;
DR	WPI; 95-098775/13.
Ţ	New human tissue inhibitor of metallo:proteinase-3 - used to
PΤ	develop prods. for diagnosis, therapy or prophylaxis of
PΤ	conditions with unwanted matrix metallo:proteinase activity.
PS	Disclosure; Fig 6A-B; 87pp; English.
ဂ္ဂ	The protein sequence of human TIMP-2 is compared with the cattle,
င္ပ	pig, human, rabbit and mouse TIMP-1, mouse and cattle TIMP-2, and
გ	chicken (Ch) and mouse TIMP-3. A probe based on the ChIMP-3
გ	amino acid sequence (R65000) is used to isolate DNA encoding
ဂ္ဂ	human TIMP-3 from a human cDNA library. Human TIMP-3 can be used
ဂ	for the diagnosis, therapy or prophylaxis of conditions
გ	characterized by excess or unwanted matrix metalloproteinase
င္ပ	activity, e.g. neoplasias, tumor metastasis, inflammatory
გ	disorders such as rheumatoid arthritis, ulcerations, reaction
င္ပ	to infection, periodontal disease or osteoporosis. It can also
ဌ	be used in drug screening/design.
SQ	Sequence 220 AA;

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Claim 8; Fig 2; 65pp; English.

Q73088 encodes R62769 human metalloproteinase inhibitor (MI), may be used to inhibit tumour cell dissemination and for treat rheumatoid arthritis, dystrophic epidermolysis bullosa, emphys and osteoporosis. The DNA may be used to detect MI gene disord Sequence 220 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-MAY-1990;
19-MAY-1989;
29-MAR-1990;
                                                                                     R07955;
21-FEB-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Metalloproteinase inhibitor; tumour cell dissemination; rheumatoid arthritis; dystrophic epidermolysis bullosa; emphysema; osteoporosis; MI gene disorders.
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R62769 stand
R62769;
13-JUL-1995
Homo sapiens.
Key
                                       scleroderma; cholesteatoma,
                                                      Human metalloproteinase inhib
Tumour; chemotherapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; Q73088.
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09-NOV-1994.
                                                                                                                                           R07955 standard;
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l Similarity 100.0%;
220; Conservative
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; US-355027.
; US-501904.
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No. 2.41e-169;
                                                    e product.
disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     olysis bullosa, emphysema
detect MI gene disorders
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                                                      osteoporosis;
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Best Local S
Matches 22
                                                                                                                                                                                   EP-623676-A.
09-NOV-1994.
18-MAY-1999; 305433
19-MAY-1989; US-355
29-MAR-1990; US-501:
(AMGE-) AMGEN INC.
(CHIL-) CHILDRENS H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein 27..220
EP-398753-A.
22-NOV-1990.
18-MAY-1990; 305433.
19-MAY-1989; US-355027.
29-MAR-1990; US-501904.
New metallo:proteinase inhibitor, analogues and treating tumour cell dissemination, rheumatoid large-scale recombinant inhibitor prodn. Claim 12; Fig 1; 65pp; English.

Q73087 encodes R62768 bovine metalloproteinase
                                                                                                                (CHIL-) CHILDRENS HOSPITAL
Boone TC, Declerck YA, La
WPI; 94-343309/43.
N-PSDB; Q73087.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 12; Fig 2; 63pp; English.

The product has therapuetic use in inhibiting tumour dissemination during chemotherapy and radiation therapy, impurged bone marrow cell harvesting etc. The inhibitor may also be useful in encapsulating tumours aiding clean excision, and in treatment of enphysema, Paget disease, osteoporosis, scleroderma and bedsores.

The gene product also has application in autoimmune disorders eg. see also Q06583.

See also Q06583.
                                                                                                                                                                                                                                                                                                                                                                                                                      Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                              emphysema;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R62768 standard;
R62768;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB, -006584
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220; Conservative
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US-355027.
US-501904.
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Pred. No. 2.41e-169;
0; Mismatches 0;
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  inhibitor
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Matches 20
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New metallo-proteinase inhibitor polypeptide(s) encoding them, for treatment of tumour cell dissenting them arthritis
                                                                                                                                                                                                                                                                                                                                                                        See also Q06584.
                                                                                                                                                                                                                                                                                                                                                                                            tumours aiding clean excision, and in treatment of enphysema, disease, osteoporosis, scleroderma and bedsores. The gene product also has application in autoimmune disorders rheumatoid arthritis and multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 12; Fig 1; 63pp; English.

The product has therapuetic use in inhibiting tumour dissemination during chemotherapy and radiation therapy, impurged bone marrow ce. harvesting etc. The inhibitor may also be useful in encapsulating
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(CHIL-) CHILDREN'S HOSPITAL OF
Langley KE, Boone TC, DeClerck
WPI; 90-350481/47.
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29-MAR-1990; US-501904.
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                                                                                                                                                                                                                                                  Score 1550;
Pred. No. 8.:
12; Mismatcl
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No. 8.23e-159;
                                                                                                                                                                                                                                             DB 2; L.
8.23e-159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dissemination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      osteoporosis;
                                                                                                                                                                                                                                                                                                 Length 220;
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                 the amino acid sequence determined. A probe was synthesised based upon the protein sequence information. It was used to screer a LambdaGem-4 cDNA library prepared from human melanoma cells. 23% positives were identified from a total of 750,000 plaques screened further analysis and screening with additional probes eliminated most of the clones. Clone pSS38 was isolated and the nucleotide sequence of the cDNA insert was determined. The deduced amino acid sequencing the TIMP-2 protein.

Sequencing the TIMP-2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R06898
Synthetic.
US7494796-A.
21-AUG-1990.
                                16-JAN-1991 (first entry)
Part of TIMP-2 metalloprot
matrix metalloproteinase i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New matrix metallo-proteinase inhibitor - used to resulting from matrix metallo-proteinase activity diagnosis, detection and purificn.

Disclosure; Fig 7; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
US7494796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           matrix metalloproteinase inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete sequence
                                                              R06896;
16-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIMP-2 was isolated from human melanoma cell-conditioned media and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (USSH ) NAT INST OF HEALTH.
Stetler-Sevenson WG, Liotta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L6-JAN-1991
                                                                                         R06896 standard;
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                                                                                                                                                                                                                                                                                                                                                     l Similarity
193; Conser
                                                                                                                                                                                                                                                                                                                                                                                                          194 AA;
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                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                   metalloproteinase
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Pred. No. 5.97e-148;
0; Mismatches 1:
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                                       inhibitor,
or; TIMP-2;
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r; TIMP-2;
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                                    encoded pss15.
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pss38.
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ls. 239
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                                                                                                                                  21-AUG-1990: 494796.

13-MAR-1989: US-326334.

21-MAR-1989: US-380431.

17-JUL-1989: US-395453.

18-AUG-1989: US-395453.

13-MAR-1990: US-494796.

(USSH ) NAT INST OF HEALTH.

StetLer-Sevenson WG, Liotta LA, KI
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21-MAR-1989; US-326334.
17-JUL-1989; US-380431.
18-AUG-1989; US-39453.
13-MAR-1990; US-494796.
(USSH) NAT INST OF HEALTH.
Stetler-Sevenson WG, Liotta LA, Krutzsch HC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PSS15.
See also Q05937,
See also Q05937,
                                                                                                                                                                                                                                                                         16-JAN-1991 (first entry)
Metalloproteinase inhibitor TIMP-2.
matrix metalloproteinase inhibitor; TIMP-2 (CSC-21K).
Synthetic.
US7494796-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnosis, detection and purificn..

Disclosure; Fig 6A; 54pp; English.

TIMP-2 was isolated from human melanoma cell-conditioned media and the amino acid sequence determined. A probe was synthesised based upon the protein sequence information. It was used to screen a Lambdagem-4 cDNA library prepared from human melanoma cells. 239 positives were identified from a total of 750,000 plaques screened. Further analysis and screening with additional probes eliminated all but two clones (pSSIS and pSSIS). Both were sequenced and found to encode CSC-21K (~TIMP-2), a novel metalloproteinase inhibitor. This is the amino acid sequence deduced from the cDNA sequence of
New matrix metallo-proteinase inhibitor - used to treat diseases resulting from matrix metallo-proteinase activity and in diagnosis, detection and purificm.

Disclosure; Fig 5; 54pp; English.

Protein was isolated from human melanoma cell-conditioned media gelatin-affinity chromatography.

It inhibits matrix metalloproteinases and can be used to treat diseases such as arthritis, diabetes, cancer, ulcers of mucosa a epithelial tissues, autoimmune-mediated inflammation, lung injur
                                                                                                                                                                                                                                                                                                                                                   R06895;
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                                                                                                                                                                                                                                                                                                                                                                  standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                              220
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larity 99.5%;
Conservative
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Pred. No. 2.
1; Mismatc
                                                                                                                                                    Krutzsch HC
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2.14e-141
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Best Local
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21 AUG-1990.
13 MAR-1999; US-326334.
21 MAR-1989; US-380431.
17 JUL-1989; US-395453.
13 MAR-1990; US-494796.
13 MAR-1990; US-494796.
USSH ) NAT INST OF HEALTH.
Stetler-Sevenson WG, Liotta L
WPI; 90-290097/38.
                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 6B; 54pp; English.

TIMP-2 was isolated from human melanoma cell-conditioned media and the amino acid sequence determined. A probe was synthesised based upon the protein sequence information. It was used to screen a LambdaGem-4 cDNA library prepared from human melanoma cells. 239 positives were identified from a total of 750,000 plaques screened. Further analysis and screening with additional probes eliminated all but two clones (pSS15 and pSS18). Both were sequenced and found to encode CSC-21K (-TIMP-2), a novel metalloproteinase inhibitor. This is the amino acid sequence deduced from the cDNA sequence of
                                                                                                                                                                                                                                                             pss18.
See also Q05937, F
Sequence 177 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; Q05939.

N-PSDB; Q05939.

New matrix metallo-proteinase inhibitor - used to new matrix metallo-proteinase activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-JAN-1991 (first entry)
Part of TIMP-2 metalloproteinase inhibitor, encoded by matrix metalloproteinase inhibitor; TIMP-2; pSS18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis, detection and purificn..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
US7494796-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R06897
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                                                               1 cscspvhpqqafcnadvvirakavsekevdsgndiygnpikriqyeikqikkfkgiekdi
aappkqefldied 192
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                                                                                                                                                                  ch 81.4%;
l Similarity 100.0%;
177; Conservative
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llarity 96.4%;
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0; Mismato
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Pred. No. 2.99e-139;
1; Mismatches 5;
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9.82e-135;
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RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          growth, osteoarthritis, osteoporosis, pulmonary emphysema, periodontal disease and rheumatoid arthritis, and for contraception. TIMP-4 cDNA can be used for gene therapy of such disorders and in diagnostic assays for TIMP-4 mRNA in cells and tissues. Oligonucleotide fragments of the TIMP-4 cDNA and antagonists or inhibitors of TIMP-4 can be used to treat disorders associated with over-expression of TIMP-4, e.g. to promote healing of corneal and diabetic ulcers and ulcers/lesions caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding a tissue inhibitor of metallo:proteinase(s), TIMP-4 for production of recombinant protein for treating tumours, arthritis, etc., and for contraception claim 1; Fig 1; 24pp; English.

This sequence is a tissue inhibitor of metalloproteinases designated TIMP-4. The CDNA clone was identified with Incyte Clone No. 589345.

TIMP-4 can be used to treat disorders associated with excessive metalloprotease expression, e.g. tumour metastasis, angiogenesis and metalloprotease expression, e.g. tumour metalloprotease expression e.g. tumour metallop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1997.
18-JAN-1996; 18-JAN-1996; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (INCY-) INCYTE PHARM INC.
Hawkins PR, Murry LE;
WPI; 97-350238/32.
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ilarity 48.2%;
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Pred. No. 2.16e-79;
53; Mismatqhes 56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 51.2%;
Best Local Similarity 48.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant TIMP-4 can be expressed in e.g. E. coli, COS or insect cell hosts. It can be used to treat patients in need of TIMP-4 (e.g. cancer, arthritic diseases, bone resportion diseases, Paget's disease, hyperparathyroidism and cholesteatoma), and to screen for antagonists useful for treating patients in need of TIMP-4 inhibition (e.g. for tissue repair and remodeling). It can also be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diseases, etc.
Claim 14; Fig 1; 49pp; English.
Human tissue inhibitor of metalloproteinase-4 (TIMP-4) (R98265)
Trs amino acid sequence
  J09235300-A
                                                                                                                                                                                          TIMP-3; human; antibody; TIMP-3-mediated cancer progression; TIMP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnostic processes.
Sequence 224 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-0CT-1996 (first entry)
Tissue inhibitor of metalloproteinase-4 (TIMP-4).
Tissue inhibitor of metalloproteinase-4; TIMP-4; cancer; arthritis;
                                                                                                                                                                                                                                                                                                                                      W30310 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             is a novel member of the TIMP family. It deduced from a cDNA clone (T34433) obtd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding human tissue inhibitor of metalloproteinase-4 (TIMP-4) useful to treat, e.g. cancer, arthritic diseases, bone resorption
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME
Greene JM, Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
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                                                     Misc-difference
                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                   Human TIMP-1/TIMP-3 fusion
                                                                                                                                                                                                                                                                                   29-JAN-1998 (first entry)
                                                                                                                                                                                                                                                                                                              W30310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; T34433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 96-300644/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-DEC-1994; U14498.
13-DEC-1994; WO-U14498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
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                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human brain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 tdwllerklygyqaqhyvcmkhvdgtcswyrghlplrkefvdivqp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 qvlsdgkvfihlckyiepwedlslvqreslnhhyhlncgcqittcytvpctisapneclw :|||: | | || :| || ||:|:|||
                                                                                                                                                                                                                                                                                                                                                                                                                                                         175 mdwvtekninghqakffacikrsdgscawyrgaappkqefldiedp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 kaegdgkmhitlcdfivpwdtlsttqkkslnhryqmgceckitrcpmipcyisspdeclw
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a cunn clone (T34433) obtd. from an early stage
The sequence shows 48% identity to human TIMP-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapy.
                                                                                                                                     Location/Qualifiers
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                          /note-
                                                                                /note= "TIMP-1 fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Mat_protein
                                                                                                                                                                                                                                                                                                                                            Protein; 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Sig_peptide
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                                                                                                                                                                                                                                                      protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 842; DB 18; 1
Pred. No. 3.61e-79;
52; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Its amino acid sequence
                                                                                                                                                                                                                        disease; malignant tumour cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 224;
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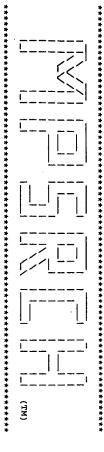
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human TIMP-3 and anti-human TIMP-3 monoclonal antibodies - used diagnosis of TIMP-3 mediated diseases, especially the detection malignant tumour cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-SEP-1997.
29-FEB-1996; 067484.
29-FEB-1996; JP-067484.
(FUJY) FUJI PHARM IND CO LTD.
WPI; 97-498341/46.
cancer, inflammation, emphysema, embcell disorders, etc.
cell disorders, etc.
Claim 3, page 66-67; 112pp; English.
The product (R84215) of Timp3clone7
                                                                                                                                        Koski RA, Silbige
WPI; 95-155259/20.
N-PSDB; T02359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-FEB-1996 (first entry)
TIMP-3 clone-7 product.
TIMP-3; tissue inhibitor metalloproteinase type three;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                        New tissue inhibitor metallo:proteinase
                                                                                                                                                                                                                                           04-OCT-1994; U11241.
06-OCT-1993; US-134231.
                                                                                                                                                                                                                                                                                                                                   WO9509918-A1.
                                                                                                                                                                                                                                                                                                                                                                                      modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R84215 standard;
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                                                                                                                                                                                              (AMGE-) AMGEN INC.
Koski RA, Silbiger SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dystrophic epidermolysis bullosa; peridontal disease; ulcer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nflammation; emphysema;
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184..186
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Pred. No. 2.:
52; Mismatcl
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     cDNA clone (T02359) is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 25; I
1.16e-65;
ches 55;
                                                                                  type three implant mov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        orthopaedic disorders, osteoporosis, autoimmune diseases and continuous diseases and continuous applications include as medicinal components of cosmetic topical compositions. Antibodies to TIMP-3 may be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disorders, infection, opthalmic disorders, corneal ulceration, orthopaedic disorders, osteoporosis, autoimmune diseases and c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inflammation, arthritis, cancer
Claim 6; Page 39; 56pp; English.
TIMP-3 is useful in the treatment of inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-APR-1995.
07-OCT-1994; U11599.
07-OCT-1993; US-133956.
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TIMP-3 can be expressed in prokaryotic
and used to treat degradative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding human monocyte/macrophage metallo:proteinase inhibitor useful e.c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          osteoporosis; autoimmune diseases; topical composition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R72598;
09-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   connective tissue disorders, periodontal disease, dermatological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; Q86744.
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Pred. No. 7.
56; Mismatc
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Pred. No. 7.60e-63;
56; Mismatches 55;
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diseases of connective tissues.
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Best Local Similarity 43.9%;
Matches 93; Conservative
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12-AUG-1994; U09188.
12-AUG-1993; US-105263.
13-DEC-1993; US-167463.
(REGC) UNIV CALIFORNIA.
Hawkes SP, Kishnani NS,
WPI; 95-098775/13.
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New human tissue inhibitor of metallo:proteinase-3 - used to develop prods. for diagnosis, therapy or prophylaxis of conditions with unwanted matrix metallo:proteinase activity. Disclosure: Fig 11: 87pp; English.

Human TIMP-3 can be used for the diagnosis, therapy or prophylaxis of conditions characterized by excess or unwanted matrix metalloproteinase activity, e.g. neoplasias, tumor metastasis, inflammatory disorders such as rheumatoid arthritis, ulcerations, reaction to infection, periodontal disease or osteoporosis. It can also be used in drug screening/design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  osteoporosis. It Sequence 206 AA;
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Human tissue inhibitor of metalloproteinase (TIMP-3).
Tissue inhibitor of metalloproteinase; diagnostic; therapeutic;
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13 glllla-tll-rpadacscspvhpqqafcnadvvirakavsekevdsgndiygnpikriq 70
                                                                                                                                               khyacirqkggycswyrgwappdksiinatdp 206
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Pred. No. 5.83e-62;
54; Mismatches 53;
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                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Release 3.0.5AA John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1997 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

abular output not generated. non: Mon May 4 14:50:16 1998; MasPar time 14.00 Seconds 574.110 Million cell updates/sec

Description: Perfect Score: >R07955 (1-220) from a-geneseq.pep 1643

1 mgaaartlrlalgllllatl.....cawyrgaappkqefldiedp 220

Scoring table: PAM 150 Gap 11

120446 segs, 36531193 residues

Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Mean 43.039; Variance 80.153; scale 0.537

Statistics:

Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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A26132	JC4802	153107	C65053	I53729	147061	A26106	JC2557	146964	A35685	A33350	ZYHUEP	JC4303	JC4630	A43429	A53532	S45317	S38624	A35996	JH0683	S45683	I53415	A37128	10	;
<pre>gag-abl-pol polyprote</pre>	alkaline proteinase (CD24 precursor - rat	hydrogenase isoenzyme	metalloproteinase inh	collagenase inhibitor	metalloproteinase inh	metalloproteinase inh	TIMP-1 - sheep		metalloproteinase inh	metalloproteinase tis	matrix metalloprotein	metalloproteinase tis	metalloproteinase inh		metalloproteinase inh	metalloproteinase inh	metalloproteinase inh	*metalloproteinase inh	metalloproteinase inh	tissue inhibitor of m	metalloproteinase inh	Description	,
1.48e-01	1.08e-01	1.08e-01	3.44e-04	3.74e-39	8.86e-78	5.46e-81	2.03e-81	6.41e-83	2.39e-83	1.45e-83	3.30e-84	3.30e-84	9.74e-119	4.72e-120	4.72e-120	5.01e-122	1.14e-294	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	FIEG. NO.	

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kinase-related transf protein-tyrosine kina	chondroadherin precur	hypothetical BCR/ABL	hypothetical BCR/ABL	protein-tyrosine kina		channel associated pr	integrin beta-7 chain	histidine kinase - Ha	hypothetical protein	platelet glycoprotein	TRAP-like protein pre	homolog of Drosophila	homolog of Drosophila	putrescine transport	delta-like dlk homeot	homeotic protein dlk	c-kit-related kinase	heat-stable antigen-r	heat-stable antigen M	probable membrane pro
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ALIGNMENTS

RESULT

	Wilhelm, S.; He, C.	:
	Goldberg, G.I.; Marmer, B.L.; Grant, G.A.; Eisen, A.Z.;	#authors
	A34415 ·	REFERENCE
	##experimental_source serum-free culture medium of A2058 cells	##experi
	123-149,'Q',151-174,'T',176-219 ##label ST2	
	is 27-77,'K',79-81,'I',83-100,'E',102-117;119-121,'R',	##residu
	e_type protein	##molecu
	A34464	#accession
	#cross-references MUID:90008902	#cross-refe
	of the metalloproteinase inhibitor family.	,
	Tissue inhibitor of metalloproteinase (TIMP-2). A new member	#title
	J. Biol. Chem. (1989) 264:17374-17378	#journal
	Stetler-Stevenson, W.G.; Krutzsch, H.C.; Liotta, L.A.	#authors
	A34464	REFERENCE
	mental_source fetal aorta cDNA library	##exper1
	ferences GB:M32304;	##Cross-
	25 1-220 ##label BOO	##residues
	##molecule_type mRNA	##molecu
	B35996	#accession
	#cross-references MUID:90207285	#cross-refe
	related to tissue inhibitor of metalloproteinases.	
	cDNA cloning and expression of a metalloproteinase inhibitor	#title
	Proc. Natl. Acad. Sci. U.S.A. (1990) 87:2800-2804	#journal
	Boone, T.C.; Johnson, M.J.; De Clerck, Y.A.; Langley, K.E.	#authors
	A35996	REFERENCE
	##experimental_source A2058 melanoma cell cDNA library	##experi
	##cross-references GB:J05593; NID:g339706; PID:g339707	##cross-
	S 1-220 ##label STE	##residues
	##molecule_type mRNA	##molecu
	A37128	#accession
	#cross-references MUID:90338014	#cross-refe
	expression in tumor cell lines and human tumor tissues.	
	Tissue inhibitor of metalloproteinases-2 (TIMP-2) mRNA	#title
	J. Biol. Chem. (1990) 265:13933-13938	#journal
	Liotta, I.A.	*aucitor a
	A3/1440	大きなは大きなこと
	\$58794	
	A37128; B35996; A34464; A34415; S21303; S20319; S17165;	ACCESSIONS
	05-Sep-1997	
	08-Mar-1991 #sequence revision 12-Apr-1996 #text change	DATE
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chon		TITLE
	A37128 #type complete	ENTRY

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159-164,172-193
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#title Isolation and characterization of tissue inhibitors of metalloproteinases (TIMP-1 and TIMP-2) from human rheumatoid synovial fluid.
#cross-references MUID:92111776
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ap_position 17q25-17q25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##status preliminary
##molecule_type protein
##residues 27-37 ##lab
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##molecule_type protein
**-caidues 27,'X',29,'X',31-38 ##label
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##residues 'X',28,
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##residues 30-51;124-141;159-173 ##label GOL
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        220;
    h 100.0%;
Similarity 100.0%;
220; Conservative
                                                                                                                                                                                                                                                                                                                regulation of extracellular matrix remodeling by inhibition of matrix metalloproteinases; TIMP-1 and TIMP-2 complex specifically with progelatinase B and progelatinase A, respectively, possibly controlling their activation; TIMP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Takahashi, K.; Takigawa, M.
Biochim. Biophys. Acta (1995) 1245:1-8
Purification of an angiogenesis inhibitor from culture medium conditioned by a human chondrosarcoma-derived chondrocytic cell line, BCS-2/8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S58794
Ohba, Y.; Goto, Y.; Kimura,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ward, R.V.; Hembry, R.M.; Reynolds, J.J.; Murphy, Blochem. J. (1991) 278:179-187
The purification of tissue inhibitor of metallopring its 72 kDa progelatinase complex.
                                                                                                                                                                                                                                                        and TIMP-2 possess erythroid potentiating activity *superfamily metalloproteinase inhibitor erythropoiesis; extracellular matrix; metalloproteinase
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                                                                                   #length
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                                                                             #disulfide_bonds #status predicted
th 220 #molecular-weight 24399 #
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#product metalloproteinase inhibitor 2 #status
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    Pred.
                                       Score 1643;
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Similarity 98.2%;
                $45683; $20325; $60160
$45683
                                                 metalloproteinase inhibitor 2 precursor - ratALTERNATE_NAMES #formal_name Rattus norvegicus #common_name Norway rat 10-Dec-1994 #sequence_revision 10-Nov-1995 #text_change
                                                                                                         S45683
                                                                                                                                                                                                                                                                                                                                                                                                                         #superfamily #length 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Martelli, M.L.; Salvatore, D.; Fusco, A.

Exp. Cell Res. (1994) 213:398-403

Cloning of the rat tissue inhibitor of metalloproteinases

type 2 (TMP-2) gene; analysis of its expression in norm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tissue inhibitor of metalloproteinase type 02-Aug-1996 #sequence_revision 02-Aug-1996
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Martelli, M.L.;
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                                        12-Apr-1996
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  T.F.; Burke, J.S.;
                                                                                                      *type complete
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 Bergman, K.D.;
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Fusco,
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39-152, 154-201,
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Local Similarity 98.2%;
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Arch. Biochem. Biophys. (1994) 311:313-320
Cloning and regulation of rat tissue inhibitor of
metalloproteinases-2 in osteoblastic cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ROSWIT, W.T.; McCourt, D.W.; Partridge, N.C.; Jeffrey, Arch. Biochem. Biophys. (1992) 292:402-410 purification and sequence analysis of two rat tissue inhibitors of metalloproteinases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Da
Rat tissue inhibitor of
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metalloproteinase inhibitor 2 precursor - mouseALTERNATE_NAMES #formal_name Mus musculus #common_name house mouse 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
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#superfamily metalloproteinase inhibitor
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##residues 27-46,'HIX',50-52,'LX',55-56,'DXX',60,'X',62 ##label KI2
##note this sequence has been revised in reference S18428
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##residues 1-11,'H',13-20,'L',22-194,'E',196-220 ##label LEC
##cross-references GB:M93954; NID:g202053; PID:g202054
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##residues 27-46,'H',48,50-53,'VD',56,'DY' ##label KIS
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214;
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JH0683; JC1234
JH0683
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Differential regulation of TIMP-1 and TIMP-2 mRNA expression in normal and Ha-ras-transformed murine fibroblasts.
                                                                                                                                                                                                                                                                                                                                                                             specifically with progelatinase B and progelatinase A, respectively, possibly controlling their activation; TIMP-1 and TIMP-2 possess erythroid potentiating activity #superfamily metalloproteinase inhibitor erythropoiesis; extracellular matrix; metalloproteinase
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Purification and characterization of a new tissue
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#title cDA cloning and expression of a metalloproteinase inhibitor feross-references MUID:90207285
#accession A35996
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27-41,'C',43-55,'EX',58-59,'X',61-66,'XS',69-71 ##label
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##residues 27-71 ##label DEC
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##cross-references GB:M32303; NID:g163341; PID:g163342
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                                                                                                                                                                 regulation of extracellular matrix remodeling by inhibition of matrix metalloproteinases; TIMP-1 and TIMP-2 complex specifically with progelatinase B and progelatinase A, respectively, possibly controlling their activation; TIMP
                                                                                                           and TIMP-2 possess erythroid potentiating activity superfamily metalloproteinase inhibitor erythropoiesis; extracellular matrix; metalloprotein
                                                                                                                                                                                                                                                                       annotation;
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Characterization of the functional domain of tissue inhibitor of metalloproteinases-2 (TIMP-2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Purification and partial amino acid sequence of a bovine
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130-177,135-140,
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39-152,154-201,
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122 HRYQMGCECKITRCPMIPCYISSPDECLWMDWVTEKSINGHQAKFFACIKRSDGSCAWYR 181
                                   86 lefiytapssavcgvsldvggkkeyllagkaegdgkmhitlcdfivpwdtlsttgkksln 145
                                                       62 IBFIYTAPSSAVCGVSLDVGGKKEYLIAGKABGDGKMHITLCDFIVPWDTLSTTQKKSIN 121
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                                                                                                                                                                                                                                                                           #disulfide_bonds #status predicted
#length 196 #checksum 7766
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06-Jan-1995 #sequence_revision 12-Apr-1996 #text_change
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#length 220 #molecular-weight 24355 #checksum
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#label MAT\
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Pred. No. 1.14e-294;
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Pred. No. 0.00e+00;
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| 206 gaappkqefldiedp 220
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##experimental_source fibroblast cell line WI-38
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##molecule_type mRNA
1-15,'W',17,'T',20-21,'PR',24-201,'X',203-211 ##label
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##cross-references EMBL:X76227; NID:g495251; PID:g495252
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Cloning of cDNAs encoding human TIMP-3, a novel member of the
tissue inhibitor of metalloproteinase family.
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                                                  Apte, S.S.; Mattei, M.G.; Olsen, B.R. Genomics (1994) 19:86-90 Genomics (1994) 19:86-90 metalloproteinases-3 (TIMP-3) and mapping of the TIMP3 gene
                                                                                                                                                                                                                                                                                                                                                 J. Biol. Chem. (1994) 269:18953-18960
A novel member of human tissue inhibitor of
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Mueller, R.
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Hawkes,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N.S.; Staskus, P.W.; Yang, T.T.; Masiarz, F.R.;
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                                                                      RESULT
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36-143,145-192,
150-155,163-184
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#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #journal DNA Cell Biol. (1994) 13:711-718
#title Cloning and characterization of 1
#cross-references MUID:95290091
#accession 153025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##cross-references GDB:138175; OMIM:188826
#map_position 22q12.1-22q13.2
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*#cross-references GB:L15078; NID:g407034; P:

##experimental_source placenta cDNA library

NNCE A56937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##residues
                                                                                                                                                              174 YPGYQSKHYACIRQKGGYCSWYRGWAPPDKSIINATDP 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##molecule_type protein
##residues 'X',25,'X',27-35,'X',37 ##label
                                                                                                                                         183 inghqakffacikrsdgscawyrgaappkqefldiedp 220
                                                                                                                                                                                                                                123 hitlcdfivpwdtlsttqkkslnhryqmgceckitrcpmipcyisspdeclwmdwvtekn 182
                                                                                                                                                                                                                                                                             114 YTGLCNEVERWDQLTLSQRKGLNYRYHLGCNCKIKSCYYLPCEVTSKNECLWTDMLSNEG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42.3%;
Local Similarity 43.6%;
hes 95; Conservation
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                                                                                                                                                                                                                                                                                                                        65 pikriqyeikqikmfkg-pek-diefiytapssavcgvsldvggkkeyliagkaegdgkm
                                                                                                                                                                                                                                                                                                                                                                     60 -L--V-YTIKQMKMYRGFTKMPHVQYIHTEASESLCGLKLEVN-KYQYLLTGRVY-DGKM 113
                                                                                                                                                                                                                                                                                                                                                                                                             7 tirlalgilila-til-rpadacscspvhpqqafcnadvvirakavsekevdsgndiygn 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 TPWLGLIVILGSWSLGDWGAEACTCSPSHPQDAFCNSDIVIRAKVVGKKLVKEGP--FGT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transcription induced by cytokines, tumor promoters,
anti-inflammatory agents
TIMP-1 and TIMP-3 have distinct but overlapping
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J. Biol. Chem. (1995) 270:14313-14318
The gene structure of tissue inhibitor of metalloproteinases
(TIMP)-3 and its inhibitory activities define the distinct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tissue-specific expression patterns #superfamily metalloproteinase inhibitor extracellular matrix; metalloproteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wilde, C.G.; Hawkins, P.R.; Coleman, R.T.;
metalloproteinase inhibitor 3 precursor - mouseALTERNATE_NAMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #disulfide_bonds #status predicted
#length 211 #molecular-weight 24145 #
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                                                 A53532
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#product metalloproteinase inhibitor 3 #status
experimental #label MAT\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translated from GB/EMBL/DDBJ
                                            #type complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 695; DB 1;
Pred. No. 5.01e-12
56; Mismatches 5
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NID:g998825; PID:g998826
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#formal_name Mus musculus #common_name house

mouse

TIMP

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                                                       CLASSIFICATION KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                #title Gene encoding a novel murine tissue inhibitor of metalloproteinases (TIMP), TIMP-3, is expressed in developing mouse epithelia, cartilage, and muscle, located on mouse chromosome 10.

#cross-references MUID:95036582
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##residues 1-211 ##label APT
##cross-references GB:L19622; NID:9438810; PID:9438811; GB:U26433;
GB:U26434; GB:U26435; GB:U26436; GB:U26437;
NID:91167532; PID:91167534
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'X',25,'X',27-34 ##label AP2
##note
a soluble recombinant form if
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##cross-references GB:L27424; NID:g439881; PID:g439882
##note not glycosylated when expressed by mon
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                                                                                                                                                                                              regulation of extracellular matrix remodeling by inhibition
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TIMP-1 and TIMP-3 have distinct but overlapping
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The gene structure of tissue inhibitor of metalloproteinases (TIMP)-3 and its inhibitory activities define the distinct
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Cancer Res. (1994) 54:1139-1144
Molecular cloning of five mesnger RNAs differentially
expressed in preneoplastic or neoplastic JB6 mouse
epidermal cells: one is homologous to human tissue
inhibitor of metalloproteinases-3.
                                                  tissue-specific expression patterns #superfamily metalloproteinase inhibitor extracellular matrix; metalloproteinase
                                                                                                                                                          transcription induced by cytokines,
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                                                                                                                                                                                   of matrix metalloproteinases
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  domain signal sequence #status predicted #label
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                                                                                                                                                                                                                                                                                                             RES
NID:g438810; PID:g438811
                                             metalloproteinase inhibitor
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                                                                                                                                                       tumor promoters,
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36-143,145-192,
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                                                                                                                                                                                                                 ##residues 26-51,'I',53 ##label STA
##experimental_source cultured embryonic
                                                                                                                                                                                                                                      ##molecule_type protein
##residues 26-51,''
                                                                                                                                                                                       ##note
                                                                                                                                                                                                                                                                                                                                                                                                                                         ##residues 1-212 ##label PAV ##cross-references GB:M94531; NID:g211901; PID:g211902 ##experimental_source ten-day old embryo cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##molecule_type mRNA 1-212 ##label
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 YTGLCNFYERWDHLTLSQRKGLNYRYHLGCNCKIKSCYYLPCFYTSKNECLWTDMLSNFG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 pikriqyeikqikmfkg-pek-diefiytapssavcgvsldvggkkeyliagkaegdgkm
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                 tissue-specific expression patterns
#superfamily metalloproteinase inhibitor
                                                                                                                                                                                                                                                                                                         Staskus, P.W.; Masiarz, F.R.; Pallanck, L.J.; Hawkes, J. Biol. Chem. (1991) 266:449-454
The 21-kDa protein is a transformation-sensitive metalloproteinase inhibitor of chicken fibroblasts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pavloff, N.; Staskus, P.W.; Kishnani, J. Biol. Chem. (1992) 267:17321-17326 A new inhibitor of metalloproteinases A third member of the TIMP family.
     extracellular matrix;
                                                 TIMP-1 and TIMP-3 have distinct but overlapping
                                                                                       of matrix metalloproteinases transcription induced by cytokines,
                                                                                                                          regulation of extracellular matrix remodeling by inhibition
                                                                                                                                                                                                                                                                                A39043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #formal_name Gallus gallus #common_name chicken 04-Mar-1993 #sequence_revision 12-Apr-1996 #tex 05-Sep-1997
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                                                                        anti-inflammatory agents
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                                                                                                                                                                               contains disulfide bonds; not glycosylated;
                                                                                                                                                                                                                                                                                                                                                                                                                          sequence extracted
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jth 211 #molecular-weight 24182 #.
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experimental #label MAT\
                                                                                                                                                                inhibitory activity
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                                                                                                                                                                                                    sarcoma virus
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Pred. No. 4.72e-120
56; Mismatches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complete
 glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                          from NCBI backbone
                                                                                                                                                                                                                   fibroblasts infected with Rous
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metalloproteinase
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                                                                                       tumor
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                                                                                     promoters, and
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37-144,146-193,
151-156,164-185
                                                                                                         Query Match
                                                                                                                                                                             207
                                                                                                                                                                                                                 24-211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         # journal
                                                                                                                                                                                                                                                                                                                                                                          ##experimental_source chondrosarcoma
This protein is a matrix-bound glycoprotein, that is a
the tissue inhibitor of metalloproteinase family and
                                                                                                                                                                                                                                                                                                                                                                                                                                ##residues 1-211 ##label WUI
##cross-references GB:UZ7201; NID:g971205; PID:g971206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 KGLNHRYHLGCGCKIRPCYYLPCFATSKNECIWTDMLSNFGHSGHQAKHYACIQRVEGYC 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194 SWYRGWAPPDKTIINATDP 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 y Match 41.8%;
Local Similarity 45.2%;
hes 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83 ek-diefiytapssavcgvsldvggkkeyliagkaegdgkmhitlcdfivpwdtlsttqk 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76
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                                                                                     Local
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                                                                      h 41.4%;
Similarity 42.7%;
93; Conservative
                                                                                                                                                                                                                                                                                                                                                             down-regulates matrix metalloproteinase activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wu, I.; Moses, M.A.
Gene (1996) 168:243-246
Cloning and expression of the cDNA encoding rat tissue
inhibitor of metalloproteinase 3 (TIMP-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                metalloproteinase tissue inhibitor 3 - ratALTERNATE.NAMES
#formal_name Rattus norvegicus #common_name Norway rat
10-Apr-1996 #sequence_revision 24-May-1996 #text_change
08-Sep-1997
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extracellular matrix; glycoprotein; meta
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#binding_site carbohydrate (Asn) (c
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#product metalloproteinase inhibitor 3 #status
experimental #label MAT\
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#product metalloproteinase tissue inhibitor 3 #status
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                                                                  Score 686; DB 1; Length 212; Pred. No. 4.72e-120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##residues 1-207 ##label FOR
##cross-references GB:L37295; NID:g561545; PID:g561546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174 YPGYQSKHYACIRQKGGYCSWYRGWAPPDKSISNATDP 211
                                                                                                                   187
                                                                                                                                                          183 QSRHLACLPREPGLCTW 199
                                                                                                                                                                                                                                      123 SFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEKGF 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##experimental_source smooth muscle cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##molecule_type mRNA
                                                                                                                                                                                                128 dfivpwdt1sttqkkslnhryqmgce-ckitrcpmipcyisspdeclwmdwvtekningh
                                                                                                                                                                                                                                                                              69 iqyeikqikmfkgpekdiefiytapssavcgvsldvggkke-yliagkaegdgkmhitlc
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                                                                                                                                                                                                                                                                                                                       66 TK-MYKGFQAL-GDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQ-DGLLHITTC 122
                                                                                                                                                                                                                                                                                                                                                             10 lalgllllatllrpadacscspvhpqqafcnadvvirakavsekevdsgndiygn-pikr
                                                                                                                                                                                                                                                                                                                                                                                                     7 LASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTT-LYQRYEIKM 65
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                                                                                                                 qakffacikrsdgscaw 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This protein, a member of the tissue inhibitor of matrix metalloproteinase family, is a secreted glycoprotein which functions through formation of a 1: complex with matrix metalloproteinase and influences the proteinase activity. It has a role as a physiological molecule for limiting vascular smooth muscle cell proliferation and migration after arterial injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                      31.7%;
Similarity 41.1%;
81; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene (1995) 163:267-271 Cloning and characterization of a cDNA encoding the baboon tissue inhibitor of matrix metalloproteinase-1 (TIMP-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *superfamily metalloproteinase inhibitor extracellular matrix; glycoprotein; meta.
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metalloproteinase tissue inhibitor 1 precursor
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Pred. No. 3.30e-84;
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#cross-references_MOID:86040463
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##residues 24-44,'L',46 ##label STR
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##cross-references GB:M12670; NID:g182482; PID:g182483
##note parts of this sequence were confirmed by protein
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DNA Cell Biol. (1990) 9:479-485
Characterization of three abundant mRNAs from human ovarian
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J. Biol. Chem. (1983) 258:12252-12258
Human skin fibroblast collagenase inhibitor.
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Primary structure and cDNA cloning of human fibroblast collagenase inhibitor.
                                                     Cytokine (1991) 3:231-239
The cytokine-protease connection: identification of a 96-kD THP-1 gelatinase and regulation by interleukin-1 and cytokine inducers.
                                                                                                                                                       Van Ranst, M.; Norga, K.; Masure, S.; Proost,
Vandekerckhove, F.; Auwerx, J.; Van Damme, ;
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A93372; A93363; A23534; A20595; A35826; A48417; S20318;
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                                                                                                                                                                                                                                                                                                                                 granulosa cells.
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protein
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                                                                                                                                                       J.; Opdenakker,
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#gene ##cross-references GDB:119615; OMIM:305370 #map_position Xpll.3-Xpll.23 CLASSIFICATION #superfamily metalloproteinase inhibitor CLASSIFICATION #superfamily metalloprotein; metalloproteinase inhibitor;
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                                                                                                                                                                                                                                                                             ##experimental_source polymorphonuclear leukocytes
This protein, found in a variety of body fluids, complexes with
metalloproteinases, irreversibly inactivating them. It also
mediates erythropoiesis in vitro; but, unlike II-3, it is
species-specific, stimulating the growth and differentiation
only human and murine erythroid progenitors.
The remarkable heat stability of this protein may be due to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##molecule_type protein
##residues 24-38 #;
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##residues 'X',25,
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##experimental_source monocytic cell line THP-1
##note sequence modified after extraction from NCBI backbone
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                                                                                                                                                                                                                                                                      disulfide bond formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Triebel, S.; Blaeser, J.; Gote, T.; Pelz, G.; Schueren, E
Schmitt, M.; Tschesche, H.
Bur. J. Biochem. (1995) 231:714-719
Evidence for the tissue inhibitor of metalloproteinases-1
(TIMP-1) in human polymorphonuclear leukocytes.
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Curr. Eye Res. (1993) 12:877-883
Characterization of a human corneal metalloproteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochem. J. (1990) 268:267-274
Disulphide bond assignment in human tissue inhibitor of metalloproteinases (TIMP).
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FEBS Lett. (1992) 296:16-20
Isolation and characterization of tissue
Isolation and characterization of TIMP-2)
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#domain signal sequence #status predicted #label SIG\
#product metalloproteinase inhibitor 1 #status
experimental #label MAT\
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36-147,150-197,
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36-147,150-196,
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#accession A33350
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1-206 ##label HOR
##cross-references GB:J04712; NID:g165742; PID:g165743
##cross-references GB:J04712; NID:g165742; PID:g165743
##experimental_source hyperoxi-exposed lung of New Zealand White rabbits
##experimental_source hyperoxi-exposed lung is induced 6-fold by
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                                                                                                                                                                                                                                                                                                                                                                regulation of extracellular matrix remodeling by inhibition of matrix metalloproteinases; TIMP-1 and TIMP-2 complex
                                                                                                                                                                          tissue-specific expression patterns
#superfamily metalloproteinase inhibitor
erythropolesis; extracellular matrix; glycoprotein
                                                                                                                                                                                                                                       anti-inflammatory agents
TIMP-1 and TIMP-3 have distinct but overlapping
                                                                                                                                                                                                                                                                                  and TIMP-2 possess erythroid potentiating activity transcription induced by cytokines, tumor promoters, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hyperoxic exposure alters gene expression in the lung. Induction of the tissue inhibitor of metalloproteinases mRNA and other mRNAs.
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J. Biol. Chem. (1989) 264:7092-7095
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larity 41.1%;
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respectively, possibly controlling their activation; TIMP-1
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Pred. No. 3.30e-84;
39; Mismatches 70
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##residues 24-37 ##label KAC
##experimental_source culture medium of fibroblastic
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##residues 24-52,'
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##cross-references GB:M60073; NID:g163760; PID:g163761
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Local Similarity 40.1%;
hes 79; Conservation
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                                                                                                                                                                    Bio/Technology (1987) 5:595-598
Molecular cloning and synthesis of biologically active human tissue inhibitor of metalloproteinases in yeast.
Moses, M.A.; Sudhalter, J.; Langer, R. Science (1990) 248:1408-1410 Identification of an inhibitor of neovascularization
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21-Sep-1990 #sequence_revision 12-Apr-1996 #text_change
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Pred. No. 1.45e-83;
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#title Tissue inhibitor of metalloproteinases (TIMP-1) produced by
granulosa and oviduct cells enhances in vitro development
of bovine embryo.
#cross-references_MUID:94257757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            155-160,168-189
53,101
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36-147, 150-197,
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        #authors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 QSRHLACLPREPGLCTW 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 SFVAPWNSMSSAQRRGFTKTYAAGCEECTVFPCSSIPCKLQSDTHCLWTDQLLTGSDKGF 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##molecule_type mRNA
##residues 1-207 ##label SAT
##cross-references GB:S70841; NID:g546973; PID:g546974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##experimental_source cartilage
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##residues 24-51 ##label MOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 iqyeikqikmfkgpekdiefiytapssavcgvsld\ggkke-yliagkaegdgkmhitlc 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 TK-MFKGFSALRDAP-DIRFIYTPAMESVCGYFHRSQNRSEEFLIAGQL-SNGHLHITTC 122
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Local Similarity 39.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 MASGILLLLMUTAPSRACTCVPPHPQTAFCNSDVVIRAKFVGTAEVNE-TALYQRYEIKM 65
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TIMP-1 and TIMP-3 have distinct but overlapping
tissue-specific expression patterns
#superfamily metalloproteinase inhibitor
erythropoiesis; extracellular matrix; glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          regulation of extracellular matrix remodeling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of matrix metalloproteinases; TIMP-1 and TIMP-2 complex specifically with progelatinase B and progelatinase A, respectively, possibly controlling their activation; TIMP-1 and TIMP-2 possess crythroid potentiating activity transcription induced by cytokines, tumor promoters, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A34833
                                                                                        I46964
                                                                                                                                                                TIMP-1 - sheepORGANISM
21-Feb-1997 #sequence_
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Smith, G.W.; Goetz, T.L.; Anthony, R.V.; Smith, M.F.
                                                                                                                                                                                                                                                                                                146964
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                                                                                                                          09-May-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #disulfide_bonds #status predicted\
#binding_site carbohydrate (Asn) (compared to the compared to the com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #domain signal sequence #status predicted #label SIG\
#product metalloproteinase inhibitor 1 #status
experimental #label MAT\
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                                                                                                                                                                                                                                                                                       #type complete
                                                                                                                                                            #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #molecular-weight 23031 #checksum 7873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 517; DB 1; Length 207; Pred. No. 2.39e-83; 42; Mismatches 70; Indels
                                                                                                                                                            #formal_name Ovis sp. #common_name shee;
21-Feb-1997 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (covalent) #status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                      Query Match 31.3%;
Best Local Similarity 39.2%;
Matches 76; Conservative
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#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               *cross-references MUID:94102210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                      ##molecule_type mRNA
##residues 1-207 ##label SMI
##residues 1-207 ##label SMI
##residues 1-207 ##label SMI
##COSS-references GB:S67450; NID:g456989; PID:g456990
##COSTION #superfamily metalloproteinase inhibitor
#FICATION #superfamily metalloproteinase inhibitor
##COSTION #SUPERFAMILY ##Olecular-weight 23057 #chec
                                           186 HLACLPREPGMCTW 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##status
190 ffacikrsdgscaw 203
                                                                                  131 vpwdtlsttqkkslnhryqmgce-ckitrcpm1pcy1sspdeclwmdwvtekninghqak 189
                                                                                                                             126 APWNSMSSAQRRGFTKTYAAGCEECTVFPCSSIPCKLQSDTHCLWTDQLLTGSDKGFQSR 185
                                                                                                                                                                                                                                                           72 eikqikmfkgpekdiefiytapssavcgvsldvggkke-yliagkaegdgkmhitlcdfi 130
                                                                                                                                                                                                                        8
                                                                                                                                                                                                                    MFKGFSALRDAP-DIRFIYTPAMESVCGYFHRSQNRSEEFLIAGQL-SNGHLHITTCSFV 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             I46964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Endocrinology (1994) 134:344-352
Molecular cloning of an ovine ovarian tissue inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      metalloproteinases: ontogeny of messenger ribonucleic a expression and in situ localization within preovulatory follicles and luteal tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                    Score 515; DB 2;
Pred. No. 6.41e-83;
42; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                      69;
                                                                                                                                                                                                                                                                                                                                                                                             Length 207
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Search completed: Mon May 4 14:50:46 1998 Job time: 30 secs.

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Release 3.0.5AA John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1997 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

no on: oular output not generated. Mon May 4 14:51:04 1998; MasPar time 15.16 Seconds 610.953 Million cell updates/sec

Description: Perfect Score: Sequence:

>R07955 (1-220) from a-geneseq.pep 1643

1 mgaaartlrlalgllllatl.....cawyrgaappkqefldiedp 220

Scoring table: PAM 150 Gap 11

Searched:

140555 seqs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb15
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 43.550; Variance 66.095; scale 0.659

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

4 5	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	44
87	87	87	87	89	89	88	88	88	88	89	89	89	89	89	89	89	89	89	89	89	89	89	89	,
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895				1149									182											
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Q91225	Q91227	009182	Q23275	Q13869	Q13870	030411	Q62208	Q37993	034234	Q13692	Q61252	Q61254	Q61255	Q61253	Q13690	Q14020	Q13848	Q61261	Q13915	P97896	Q13691	Q61260	Q61259	K H C E U -
GLUTAMATE RECEPTOR SUB	GLUTAMATE RECEPTOR SUB	INTEGRIN BETA-7 SUBUNI	SIMILAR TO S. CEREVISI	PROTO-ONCOGENE TYROSIN	PROTO-ONCOGENE TYROSIN	PUTATIVE ABC-TRANSPORT	STROMAL CELL DERIVED P	MAJOR HEAD PROTEIN.	SUGAR TRANSFERASE.	BCR/ABL FUSION PROTEIN	•	PROTEIN,	C-ABL PROTEIN, TYPE II	C-ABL PROTEIN, TYPE II	HYPOTHETICAL PROTEIN (BCR/C-ABL ONCOGENE PRO	BCR/C-ABL ONCOGENE PRO	ABELSON MURINE LEUKEMI	C-ABL (FRAGMENT).	ABELSON MURINE LEUKEMI	ABL PROTEIN (FRAGMENT)	ABELSON MURINE LEUKEMI	ABELSON MURINE LEUKEMI	***************************************
1.52e+00	1.52e+00	1.52e+00	1.52e+00	7.51e-01	7,51e-01	1.07e+00	1.07e+00	1.07e+00	1.07e+00	7.51e-01	7.51e-01	7.51e-01	7.51e-01	7.51e-01	7.51e-01	7.51e-01	7.51e-01	7.51e-01	7.51e-01		.51e	7.51e-01	7.51e-01	C. EUC C.

ALIGNMENTS

RESULT ID O	Оў	рь Оу	ор Оу	Ωу	Ma Ma	RA PET	AC OC OC DT TT AC	RESULT ID Q
DLT 2 042146 PRELIMINARY; PRT; 220 AA.	182 GAAPPKQEFLDIEDP 196 	122 HRYQMGCECKITRCPMIPCYISSPDECLWMDWYTEKSINGHQAKFFACIKRSDGSCAWYR 181 	62 IEFIYTAPSSAVCGVSLDVGGKKEYLIAGKAEGDGKMHITLCDFIVPWDTLSTTQKKSLN 121 	2 ACSCSPVHPQQAFCNADVVIRAKAVSEKEVDSGNDIYGNPIKRIQYEIKQIKMFKGPDKD 61 	Query Match 89.2%; Score 1466; DB 10; Length 196; Best Local Similarity 99.0%; Pred. No. 0.00e+00; Matches 193; Conservative 2; Mismatches 0; Indels 0; Gaps		Q60453; Q1-NOY-1996 (TREMBLREL. 01, CREATED) Q1-NOY-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE) Q1-JAN-1996 (TREMBLREL. 05, LAST ANNOTATION UPDATE) Q1-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE) TISSUE INHLBITOR OF METARO PROTEINASE (FRAGMENT). CRICETULUS LONGICAUDATUS (LONG-TAILED HAMSTER). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; RODENTIA. [1] SEQUENCE FROM N.A.	Q60453 PRELIMINARY; PRT; 196 AA.

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Matches 10
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01-MAY-1997
01-MAY-1997
01-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1997 (TREMBLREL. 03, CREATED)
01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
01-MAY-1997 (TREMBLREL. 03, LAST ANNOTATION UPDATE)
TISSUE INHLBITOR OF METALLOPROTEINASE 4.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA.
                                                                                                                                                                                                                                                           GREENE J., WANG M., RAYMOND L.A., LIU Y.E., ROSEN C., SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS. EMBL; U76456; G1773293; CSEQUENCE 224 AA; 25502 MW; EAF29A49 CRC32;
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE-HEART;
                                                                                                                                                                                                                                                                                                                                                                                                                 EUKARYOTA; METAZOA;
EUTHERIA; PRIMATES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GALLUS (CHICKEN).
EUKARYOTA; METAZOA; CHOR
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01-JAN-1998 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
TISSUE INHIBITOR OF META
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIMP-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
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        57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ω
                                                                                MPGSPRPAP-SWVLLLRLLALLRPPGLGEACSCAPAHPQQHICHSALVIRAKISSEKVVP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sgndiygnpikriqyeikqikmfkgpek--diefiytapssavcgvsldvggkkeyliag
                    ASADP-ADTEKMLRYEIKQIKMFKGFEKVKDVQYIYTPFDSSLCGVKLEANSQKQYLLTG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KMHITLCDLVATWDSVSPTQKKSLNQRYQMGCECKISRCLSIPCFVSSSDECLWTDWAME 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAALPSL-LAWLAVLLLGRA-RPADACSCSPIHPQQAFCNADVVIRAKRVSAKEVDSGND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 79.9%;
l Similarity 78.6%;
173; Conservative
                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS00288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1
27
220
                                                                                                                                                                        51.4%;
llarity 48.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ĀĀ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 P
220 T
24313 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIMP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               METALLOPROTEINASE-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   888
                                                                                                                                                                        Score 844; DB 2; L
Pred. No. 4.37e-190;
53; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CREATED)
LAST SEQUENTIAL LAST ANNOTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred.
22; }
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1313; DB 12; Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
TISSUE INHIBITOR OF
; F477B394 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE UPDATE)
ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                   TETRAPODA;
                                                                                                                                                                                                                Length 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METALLOPROTEINASE-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 220;
                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QUIGLEY
                                                                                                                                                                                                                                                                                                                                                                                                                                   MAMMALIA;
                                                                                                                                                                                                                                                                                                                     Y.E.;
                                                                                                                                                                      8,
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                                                                                                                                                                   Gaps
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ID P70533
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  Query Match
                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                SEQUENCE FROM N.A.

TISSUE-LIVER;
IREDALE J.P., BENYON R.C., ART
WINWOOD P.J., CLARK N., MURCHY
HEPATOLOGY 24:176-184(1996).
EMBL; L29512; G1550734; -.
                  EMBL; L29
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1997
01-JUL-1997
01-JAN-1998
                                                                                                                                        01-FEB-1997 (TREMBLREL.
01-FEB-1997 (TREMBLREL.
01-FEB-1997 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LT 4
002722
                                                                                                EUTHERIA;
                                                                                                        EUKARYOTA;
                                                                                                                RATTUS NORVEGICUS
                                                                                                                                 METALLOPROTEINASE INHIBITOR
                                                                                                                                                                     P70533;
                                                                                                                                                                                                                                                                                                                                                                                                              RICHARDSON D.W., DODGE (
SUBMITTED (MAY-1997) TO 
EMBL; U95039; G2072247; 
PROSITE; PS00288; TIMP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQUUS CABALLUS (HORSE).
EUKARYOTA; METAZOA; CHORDATA;
EUTHERIA; PERISSODACTYLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIMP-1.
                                                                                                                                                                                                                          183
                                                                                                                                                                                                                                         179
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE INHIBITOR
                                                                                                                                                                                                                                                            124
                                                                                                                                                                                                                                                                             119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 TDWLLERKLYGYQAQHYVCMKHVDGTCSWYRGHLPLRKEFVDIVQP
                                                                                                                                                                                                                                                                                               70
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                                                                                                                                                                                                                                 DKGFQSRYLACLPREPGLCTW:| |:::| |:|
                                                                                                                                                                                                                                                         itlcdfivpwdtlsttqkkslnhryqmgc-eckitrcpmipcyisspdeclwmdwvtekn
                                                                                                                                                                                                                                                                           ITTCSFVAPWNSLSSAQRQGFTKTYAAGCGECSVFPCSSIPCKLQSDTDCLWTDQLLTGS
                                                                                                                                                                                                                                                                                          h 28.8%;
Similarity 39.3%;
79; Conservative
                                                                                                RODENTIA.
                   176
                                                                                                        METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                       207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TREMBLREL.)
(TREMBLREL.)
                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                (RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                        DODGE G.R.;
                  19659 MW;
                                                                                                                                                                                                                                                                                                                                                                                                     IMP; 1.
23046 MW;
                                                                                                       CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REL. 04, CREATED)
REL. 04, LAST SEQUENCE UPDATE)
REL. 05, LAST ANNOTATION UPDATE)
METALLOPROTEINASE-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                TO EMBL/GENBANK/DDBJ
                                                                                                                                        02,
                                                     MURPHY
                                                    ARTHUR M.J.,
VPHY G.;
                                                                                                                                                                                                                                         199
                                                                                                                                                                                                                        203
                                                                                                                                       LAST SEQUENCE UPDATE)
                                                                                                                                                           CREATED)
                                                                                                                                                                                                                                                                                                                                                                  Score 474; DB 4;
Pred. No. 3.95e-91;
42; Mismatches 65
                                                                                                                                  (FRAGMENT)
                                                                                                                                                                                     PRT;
                                                                                                       VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                  7CB8A5D1
                                                                                                                                                                                                                                                                                                                                                                                                     7174F434 CRC32
                                                                                                                                                                                     176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          207
 В
                  CRC32;
                                                             FERRIS
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                                                                                                                                                                                                                                                                                                                                                                                                                               DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TETRAPODA; MAMMALIA;
10;
                                                            W.F.,
                                                                                                                                                                                                                                                                                                                                                                                  Length 207;
                                                                                                                                                                                                                                                                                                                                                                                                                               BANKS
                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            224
                                                            ALCOLADO
                                                                                                                                                                                                                                                                                                                                                                  15;
                                                            R.,
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174
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Length

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                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CT 6
Q16121
                                                                                                                                                                                                                                    01-NOV-1996 (TREMBLEREL 01, CREATED)
01-NOV-1996 (TREMBLEREL 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLEREL 01, LAST ANNOTATION UPDATE)
SIMILAR TO METALLOPROTEINASE INHIBITOR 2 PRECURSORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TREMBLREL. 01-NOV-1996 (TREMBLREL. 01-JAN-1998 (TREMBLREL.
                                                            BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELIO A., FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLER L., JIER M., JOHNSTON L. JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LARREILLE P., JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LARREILLE P., LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
                                                                                                                            STRAIN-BRISTOL N2;
MEDLINE; 94150718.
WILSON R., AINSCOUGH R.,
                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                             CAENORHABDITIS ELEGANS
                                                                                                                                                                                                                                                                                          Q21265;
                                                                                                                                                                                                                                                                                                                    Q21265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 94156197.
DE CLECK Y.A., DARVILLE M.I.,
GENE 139:185-191(1994).
EMBL; 568860; E119468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       016121;
WATSON A., WEINSTOCK L., NATURE 368:32-38(1994).
                                    PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
                                                                                                                                                                                               EUKARYOTA; METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUTHERIA; PRIMATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIMP-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIMP-2-METALLOPROTEINASE-2
                     THIERRY-MIEG J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gce-ckitrcpmipcyisspdeclwmdwvtekninghqakffacikrsdgscaw 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCGVCTVFPCSVIPCKLESDTHCLWTDQILMGSEKGYQSRHLACLPRNPGLCTW 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HPQTAFCNSDLVIRAKFMGSPEI-IETTLYQRYEIKMTK-MLKGFDAV-GNATDIRFAYT 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAMESLCGYVHKSQNRREEFLIAGRLR-NGNLHITACSFLVPWASLSPAQRKGLTKTYSA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hpqqafcnadvvirakavsekevdsgndiygn-pikriqyeikqikmfkgpekdiefiyt 91
                                                                                                                                                                                                                                                                                                                                                                                                                           h 18.6%;
Similarity 100.0%;
43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 38.5%; 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS00288; TIMP; 1.
50 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50 AA;
                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                         THOMAS K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5121 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA.
                                                                                                                                                                                                ACCELOMATES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01,
            WILKINSON-SPROAT J.,
                                                                                                                               ANDERSON K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , CREATED)
, LAST SEQUENCE UPDATE)
, LAST SEQUENCE UPDATE)
, LAST ANOTATION UPDATE)
TISSUE INHIBITOR (PROMOTER (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 306; 1
Pred: No. 2.
0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4992D252 CRC32;
                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EECKHOUT
                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                               NEMATODA; SECERNENTEA; RHABDITIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No.
                                                                                                                                                                                                                                                                                                                    158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.29e-84;
                                                                                                                             BAYNES C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50
                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
.70e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Υ.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ROUSSEAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64;
            WOHLDMAN P.;
                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 50
                                                                                                                                                                                                                                                                                                                                                                                                 43
                                                                                                                             BERKS M.,
                                                                                                                                                                                                                                                                                                                                                                        43
                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                         WATERSTON R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G.G
                                                                                        JOHNSTON L.,
                                                                                                                COULSON A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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RRRRCCS BITTE
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                                                                                                                                            RESULT
                                                                                                                                                                                                                          Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [2]
SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
WU X, LE TT.;
                                                                    056365;
01-NOV-1996 (TREMBLREL. 01, CREATED)
01-FEB-1997 (TREMBLREL. 02, LAST SEQ
01-JAN-1998 (TREMBLREL. 05, LAST ANN
THERMOSTABLE ALKALINE PROTEASE.
                                                                                                                                LT 9
Q56365
                                                                                                                                                                                                                                                                                                                                                                    Q62779;
01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                       LT 8
Q62779
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

STRAIN-WISTAR; TISSUE-ISLETS OF LANGERHANS;
SYENSSON C., MICHELSEN B., BILLESTRUP N., NIELS
SUBMITTED (MAY-1995) TO EMBL/GENBANK/DDBJ DATA
EMBL; U25680; G802014; -
                                                                                                                                                                                                                                                                                                                                        RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBMITTED (APR-1996) TO EMBL/GENBANK/DDBJ EMBL; U53336; G1255824; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
 STRAIN-E79;
LEE J.K., F
                                                  THERMOACTINOMYCES SP. EUBACTERIA; FIRMICUTES;
                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                            PREADIPOCYTE FACTOR 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBMITTED
                                                                                                                                                                                                                                                                                                                               EUTHERIA;
                                         THERMOACT INOMYCES
                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 itlcdfivp 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 TVLCGQVLP 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 kriqyeikqikmfkgp-ekd-i-efiytapssavcgvsldvggkkeyliagkaegdgkmh 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U53336; G1255824;
NCE 158 AA; 174
                                                                                                                                                                                                              6.1%;
Similarity 42.6%;
20; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 12.7%;
Similarity 27.9%;
36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (APR-1996)
KIM Y.O.,
                                                                                                                                                                                                                                                        383 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                  PRELIMINARY;
 KIM
                                                                                                                                                                                                                                                        41253 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17465 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TO
                                                                                                                                                                                                                                                                                                                                                                     999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL/GENBANK/DDBJ DATA BANKS
 H.K.,
                                                  ACTINOMYCETES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 208; DB 3;
Pred. No. 7.32e-25;
40; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                    CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                          Score 100; DB 10;
Pred. No. 1.24e-02;
                                                                                                                                                                                                                                                                                                                                         VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
 PARK Y.S.,
                                                                                                                                  PRT;
                                                                                                                                                                                                                                                        58BED3DD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FBD8E38D
                                                                                                                                                                                                                Mismatches
                                                                                ANNOTATION
                                                                                          SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                         383
                                                                                                                                  384
                                                  THERMOACTINOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRC32;
 Ю
                                                                                                                                                                                                                                                                                                                                                                                                                        B
                                                                                                                                                                                                                                                                                                                                         TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DATA
                                                                                                                                                                                                                                                                                      NIELSEN J.H.;
  H
                                                                                UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43;
                                                                                                                                                                                                                                                                            BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BANKS
                                                                                                                                                                                                                                   Length 383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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FIRE RAPE OCCUPATION OF THE PRESENTATION OF TH
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ID Q
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Best Local S
Matches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 6.0%;
Best Local Similarity 40.6%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JLT 10
Q61720
                                                                                                                                                                                                                                                                                                                                                                                                                         Q95117;
01-FEB-1997 (
01-FEB-1997 (
01-JAN-1998 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEIC ACIDS RES. :
EMBL; V00755; G8179
EMBL; J00425; G1941:
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U31759; G168: PROSITE; PS00136; PROSITE; PS00137; PROSITE; PS00138; PROSITE; PS00138;
                                                                                                                                                                                                                                                                                        BOS TAURUS
EUKARYOTA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LT 11
Q95117
SEQUENCE FROM N.A.

MEDLINE; 96421609.

HOANG B., MOOS M., VUKICEVIC S., LUYTEN
J. BIOL. CHEM. 271:26131-26137(1996).

EMBL; UZ4164; G1620539; -

SIGNAL 1 25
SIGNAL 1 25
CHAIN 26 325
FRZB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       061720;
01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-FEB-1997 (TREMBLREL. 02, LAST ANNOTATION UPDATE)
MESSENGER RNA FRAGMENT FOR MOUSE INTERFERON BETA (TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THE C-TERMINAL PART (FRAGMENT).
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEERATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 82247191.
SKUP D., WINDASS J.D., SOR F.S.,
FUKUHARA H., DE MAEYER-GUIGNARD
                                                                                                                                                                                                                                                              EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                            FRZB PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U31759; G1683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 clwmdwvtekninghqakffacikrsdgscaw 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLWTDQVLVGS-EDYQSRHFACLPRNLGLCTW 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KSIEKSKYLGFEVVKFDGSVEKMIE
::|:|:||:|||||
npikriqyeikqikmfkgp-ekdie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.1%;
Similarity 27.1%;
23; Conservative
                                                                                                                                                                                                                                                           S (BOVINE).; METAZOA; CHORDATA; ARTIODACTYLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                384
                                                                                                                                                                                                                                                                                                                                                                                                                      7 (TREMBLREL.
7 (TREMBLREL.
3 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 AA; 4390 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S RES. 10:3069-3084(1982). (6817965) -. (6194118; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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SUBTILASE_HIS; 1.
SUBTILASE_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40132
                                                                                                                                                                                                                                                                                                                                                                                                                         9,2,2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 100;
Pred. No. 1.
25; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 99; DB 10;
Pred. No. 1.82e-02
7; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                               CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   429816C2 CRC32;
                                                                                                                                                                                                                                                                                            VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A3C189F5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GEORGE H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E H., WILLIAMS B.R.G., MAEYER E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 9; Le
L.24e-02;
ches 33;
                                                                                                                                F.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ä
                                                                                                                                                                                                                                                                                        TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                      UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                     MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAMMALIA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63
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RESULT
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Matches 1
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Best Local S
Matches 3
    Query Match
Best Local Similarity
Matches 20; Conser
                                                                            SEQUENCE FROM N.A.
MEDLINE; 96208959.
ISHTANI M., MAJUMDER A.L., B.
JENSEN R.G., BOHNERT H.J.;
PLANT J. 9:537-548 (1996).
EMBL; U32511; G975888; -.
SEQUENCE 512 AA; 56758 MW;
                                                                                                                                                                                                                                                                                                                              Q40271;
01-NOV-1996;
01-NOV-1996;
01-JAN-1998;
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01-NOV-1996
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Q40271
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Q61692
                                                                                                                                                                                                                                                                MESEMBRYANTHEMUM CRYSTALLINUM (COMMON EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIO:
                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TREMBLREL 01, CREATI
01-NOV-1996 (TREMBLREL 01, LAST 1
01-JAN-1998 (TREMBLREL 05, LAST 1
MYO-INOSITOL-1-PHOSPHATE SYNTHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WENGER R.H., AYANE M., BOSE R., KOEHLER G., EUR. J. IMMUNOL. 21:1039-1046(1991).
EMBL; X56486; G51442; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-CBA X C57BL/6; TISSUE-SPLEEN;
MEDLINE; 91209380.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSA-C GENE
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17; Conser
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Similarity 27.2%;
37; Conservative
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6 (TREMBLREL. 01,
6 (TREMBLREL. 01,
CODING FOR HEAT S
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  5.8%;
larity 38.5%;
Conservative
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larity 50.0%;
Conservative
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                                                                                  MW;
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, LAST SEQUENCE UPDATE)
, LAST ANNOTATION UPDAT
STABLE ANTIGEN.
Score 95; DB 8;
Pred. No. 8.35e-02
12; Mismatches 1
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Pred. No.
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Pred. No. 1.82e-02;
34; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                      CREATED)
                                                                                                                                                               BORNHOUSER
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                8F97FE26 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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  Indels
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                                          512;
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                                                           Query Match 5.5%;
Best Local Similarity 35.7%;
Matches 10; Conservative
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Best Local Similarity 31.7%;
Matches 20; Conservative
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Q91909
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MEDLINE; 97366649.
VIRGIN H.W. IV, LATREILLE P.,
DAL CANTO A.J., SPECK S.H.;
J., VIROL. 71:5894-5904(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    O41968;
01-JAN-1998
                                                                                                                          LATRELILLE P., WAMSLEY P., WATERSTON R.H.;
SUBMITTED (APR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U9753; G2317997; -
SEQUENCE 226 AA; 25881 MW; D2AD43E8 CRC32;
                                                                                                                                                                                                                                                                                                                                                     MURINE HERPESVIRUS 68.
VIRUSES; DSDNA VIRUSES,
                                                                                                                                                                                                                                                                                                                                                                                      GAMMAHV.ORF67
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01-JAN-1998
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01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 367 ELHLIRL-KGTEKGVYTFYYTTNSDDDASVSFNIQVKTRPEILIAERT-SEGTLQCVATGF 424
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83 ekdieflytapssa-vcgvsldvggkkeyliagka--egdgkmhitlcdfiv 131
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                                                                                                                                                                                                                                                                                                                                                                                                    EGUMENT PROTEIN.
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ECH. DEV. 50:217-228(1995).
MBL; Z48770; G763034; -.
                                                                                                                                                                                                          QUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQUENCE FROM N.A.
76 ikmfkgpekdieflytapssavcgvsld 103
                               92 LKCFMSPPRDIDFQYGNRVNMACDVNLE 119
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20
954 AA;
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(TREMBLREL.
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54 C-KIT-RELATED KINASE 1.
106859 MW; 3B301EB3 CRC32;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 8.35e-02;
17; Mismatches 22;
                                                           Score 90; DB 11;
Pred. No. 5.25e-01;
8; Mismatches 10
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                                                                                                                                                                                                                                                                      WAMSLEY P.,
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                                                                                           DB 11; Length 226
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                                                               10; · Indels
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Search completed: Mon May 4 14:51:34 1998 Job time: 30 secs.

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MPsrch_pp no on: protein - protein database search, using Smith-Waterman algorithm Mon May 4 14:49:45 1998; MasPar time 9.58 Seconds 575.950 Million cell updates/sec

Description:
Perfect Score:
Sequence: >R07955 (1-220) from a-geneseq.pep 1643

Jular output not generated.

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Scoring table: PAM 150 Gap 11

Searched: 69112 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

swiss-prot35 1:swiss1

Database:

Statistics: Mean 44.629; Variance 66.231; scale 0.674

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

συ Αυ ΝΗ :	1643 1630 1620 1550 695		220 1 220 1 220 1 220 1 220 1 221 1 211 1		TIM2_HUMAN TIM2_RAT TIM2_MOUSE TIM2_BOVIN TIM3_HUMAN TIM3_BOVIN	DESCRIPTION METALLOPROTEINASE INHI METALLOPROTEINASE INHI METALLOPROTEINASE INHI METALLOPROTEINASE INHI METALLOPROTEINASE INHI METALLOPROTEINASE INHI
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11		31.7	207	۲	TIM1_HUMAN	METALLOPROTEINAS
1:		31.5	206	1-	TIM1_RABIT	METALLOPROTEINASE
<u></u>		31.5	207		TIM1_BOVIN	METALLOPROTEINAS
14		31.3	207	_	TIM1_SHEEP	METALLOPROTEINASE
11		30.9	217 .	_	TIM1_RAT	METALLOPROTEINASE
1		30.8	205	_	TIM1_MOUSE	METALLOPROTEINASE
1	7 491	29.9	207	μ.	TIM1_PIG	METALLOPROTEINASE
11	8 117	7.1	290	بر	HYPB_ECOLI	HYDROGENASE ISOENZYMES
11	9 100	6.1	76	_	CD24_RAT	SIGNAL TRANSDUCER CD2
Ŋ	0 98	6.0	1025	1	YBD7_YEAST	ALPHA-ADAPTIN HOMOLOG
2	1 96	5.8	76	_	CD24_MOUSE	SIGNAL TRANSDUCER CD24
2	2 93	5.7	383	ш	DLK_HUMAN	DELTA-LIKE PROTEIN PRE
N	3 93	5.7	404	ب	POTG_ECOLI	PUTRESCINE TRANSPORT A

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
85	85	86	87	87	88	89	89	89	88	88	88	88	88	91	90	90	90	91	91	90	92
	5.2		5	5.3	5.4	5.4	٥. 4.	5.4	Մ. ♣	5.4	5.4	5.4	5.4	5.5	5.5	5 5	5.5	5.5	5	5.5	5.6
852	436	192	852	507	1415	1130	1123	1036	509	385	367	264	80	3033	870	806	361	206	173	155	904
r	\vdash	ب	<u> </u>	-	-	Н	۳	μ	ب	\vdash	Н	μ	r	۳	μ.	μ.	H	_	_	-	-
RA54_SCHPO	YRS4_CAEEL	INF_MELGA	SP93_RAT	INO1_CITPA	RPOC_HAEIN	ABL1_HUMAN	ABL_MOUSE	YG35_YEAST	SYK_ACICA	DLK_MOUSE	DIAC_RAT	TRPA_SYNY3	CD24_HUMAN	POLG_HCVJ8	SP93_HUMAN	ITB7_MOUSE	CHAD_BOVIN	GPBB_HUMAN	SSRD_HUMAN	ECP_RAT	SP97_HUMAN
DNA REPAIR PROTEIN RAD	HYPOTHETICAL 49.4 KD P	INTERFERON PRECURSOR.	CHANNEL ASSOCIATED PRO	MYO-INOSITOL-1-PHOSPHA	DNA-DIRECTED RNA POLYM	PROTO-ONCOGENE TYROSIN	PROTO-ONCOGENE TYROSIN	HYPOTHETICAL 117.0 KD	LYSYL-TRNA SYNTHETASE	DELTA-LIKE PROTEIN PRE	DI-N-ACETYLCHITOBIASE	TRYPTOPHAN SYNTHASE AL	SIGNAL TRANSDUCER CD24	GENOME POLYPROTEIN (CO	CHANNEL ASSOCIATED PRO	INTEGRIN BETA-7 SUBUNI	CHONDROADHERIN PRECURS	PLATELET GLYCOPROTEIN	TRANSLOCON-ASSOCIATED	EOSINOPHIL CATIONIC PR	PRESYNAPTIC PROTEIN SA
2.06e+00	2.06e+00	1.46e+00	1.03e+00	1.03e+00	7.26e-01	5.09e-01	5.09e-01	5.09e-01	7.26e-01	7.26e-01	7.26e-01	7.26e-01	7.26e-01	2.48e-01	3.56e-01	3.56e-01	3.56e-01	2.48e-01	2.48e-01	3.56e-01	1.72e-01

ALIGNMENTS

TIM2_HUMAN STANDARD; PRT; 220 AA. PLAGO35; O33006; O1-NOY-1990 (REL. 14, CREATED) O1-NOY-1990 (REL. 16, LAST SEQUENCE UPDATE) EUTHERIA; PRIMATES O1 (HUMAN) SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE; 90207285 BOONE T.C., JOHNSON M.J., DE CLERCK Y.A., LANGLEY K.E.; PROC. NATL. ACAD. SCI. U.S.A. 87:2800-2804(1990). [2] SEQUENCE FROM N.A. MALKK K., SELIMA H., AOKI T., IMATA K.; SUBMITTED (AUG-1990) TO EMBL/GENBANK/DDBJ DATA BANKS. [5] SEQUENCE OF 30-214 FROM N.G., KRUTZSCH H.C., LIOTTA L.A.; J. BIOL. CHEM. 264:17374-17378(1989). SEQUENCE OF 30-51; 124-141 AND 159-173. MEDLINE; 90046755. GOLDBERG GI., MARMER B.L., GRANT G.A., EISEN A.Z., WILHELM S., HE C. SEQUENCE OF 27-41. TISSUE-SYMOYIAL FUILD; MEDLINE; 9211176.

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 RESULT
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DT 0
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FEBS LETT. 296:16-20(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VILLIAMSON R.A., MARTORELL G., CAN
REEDMAN R.B., FEENEY J.;
SIOCHEMISTRY 33:11745-11759(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -I- FUNCTION: COMPLEXES WITH MET
AND IRREVERSIBLY INACTIVATE
II- PTM: THE ACTIVITY OF TIMP-2
                                                                                                                                                                                                                             mery Match
                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                   ONFLICT
TIM2_RAT
P30121;
01-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                              SULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J05593; G339707; S48568; G298202; J044385; G1517893; JOINED.
J044381; G1517893; JOINED.
J044382; G1517893; JOINED.
J044382; G1517893; JOINED.
J044383; G371893; JOINED.
J043304; G307195; J043304; G37181; J043304; G37181; J
                                                         181
                                                                           181
                                                                                          Local
                                                                                                                                  61
                                                                                                                                                    61
                                                                                                                                                                     SULFIDE BONDS
                                                                                                                                h 100.0%;
Similarity 100.0%;
220; Conservative
                                                                                                                                                                                                                                                   118
122
150
175
220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIGH WITH OTHER MEMBERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MARTORELL G., CARR M.D.,
                                                                                                                                                                                                                                                     ξ
                                                                                                                                                                                                                                                                                                                                                                                                                           INHIBITOR;
                      STANDARD;
     25, CREATED)
                                                                                                                                                                                                                                                      24399 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OBERHOFF R., REINKE H., TSCHESCHE H.;
                                                                                                                                                                                                                                                                                                                                                                     METALLOPROTEINASE INHIBITOR 2
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      METALLOPROTEINASES (SUCH AS COLLAGENASES)
                                                                                                                                                                                                                         Score 1643; DB 1;
pred. No. 0.00e+00;
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IS DEPENDENT ON THE
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                                                                                                                                                                                                                                                        834D259A CRC32;
                                                                                                                                                                                                                                                                                                                                                     SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                   Mismatches
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( (IN REF. 5).
! (IN REF. 5).
! (IN REF. 4).
! (IN REF. 5).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MURPHY G., DOCHERTY A.J.P.,
                           220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THE TIMP FAMILY.
                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                       Length 220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRESENCE
                                                                                                                                                                                                                      Indels
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01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
METALLOPROTEINASE INHIBITOR 2 PRECURSOR (TIMP-2) (TISSUE INHIBITOR OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHOR
                                                                                                                                                                                  Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-SPRAGUE-DAWLEY; TISSUE-BONE; MEDLINE; 94263207.
COOK T.F., BURKE J.S., BERGMAN K.D. PARTRIDGE N.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               METALLOPROTEINASES-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIMP2 OR TIMP-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 94326839.

SANTORO M., BATTAGLIA C., ZHANG L.,
SALVATORE D., FUSCO A.;
EXP. CELL RES. 213:398-403(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GIBBONS K.L., O'GRADY
SUBMITTED (JUN-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-MAMMARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RCH. BIOCHEM. BIOPHYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE-TESTIS;
TISSUE-TESTIS;
OBJANA J., CALCAGNO K., CHENG
GRIMA J., CALCAGNO K., CHENG
J. ANDROL. 17:263-275(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: HIGH WITH OTHER MEMBERS OF THE TIMP FAMILY.
EMBL; U14526; G540205; ".
EMBL; L31884; G1141730; ".
EMBL; S72594; G619233; ".
EMBL; S82718; G1881814; ".
                                                                                                                                                                                                                                                                                                                                                                        DISULFID DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METALLOPROTEASE
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      61
                                          61
                                                                               216;
                                                                                                                                                                                             Similarity
                                                                                                                                                                     99.2%;
llarity 98.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88; TIMP;
                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INHIBITOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHORDATA;
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220
98
127
152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .L., PIPER A.A.;
EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               311:313-320(1994).
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BY SIMILARITY.
BY SI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C.Y.;
                                                                                                                                                                         Score 1630; DB 1;
pred. No. 0.00e+00;
3; Mismatches 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IS DEPENDENT ON THE PRESENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QUINN C.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARLOMAGNO F., MARTELLI M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JEFFREY
                                                                                                                                                                                                                             Length 220;
                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ч.
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DT 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIM2_MOUSE STANDARD,

p25785;

p25785;

p1-MAY-1992 (REL. 22, CREATED)

01-MAY-1993 (REL. 25, LAST SEQUENCE UPDATE)

01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)

01-NOV-1995 (REL. 32, LAST ANNOTATION TIMP-2)

METALLOPROTELNASE INHIBITOR 2 PRECURSOR (TIMP-2)
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                                                                                                                      Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            METALLOPROTEINASES-2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 92290292.
SHIMIZU S., MALIK K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENE 117:209-217(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LECO K.J., HAYDEN L.J.,
EDWARDS D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE; 92347695.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY SEQUENCE OF 27-62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFIDE BONDS.
-!- SIMILARITY: HIGH WITH OTHER MEMBERS EMBL; X62622; G54802; -- EMBL; M82858; G202052; -- EMBL; M83954; G202054; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KISHI J.I., OGAWA K., YAMAMOTO S., MATRIX 11:10-16(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 91226375.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- FUNCTION: COMPLEXES WITH METALLOPROTEINASES
AND IRREVERSIBLY INACTIVATE THEM.
-1- PTM: THE ACTIVITY OF TIMP-2 IS DEPENDENT ON
                                                                                                                                                                                                                                                                                                      DISULFID
DISULFID
DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                             ETALLOPROTEASE
                                                                                                                                                                                                                                 CONFLICT
                             MGI:98753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   JH0683;
IYGNPIKRIQYEIKQIKMFKGPDKDIEFIYTAPSSAVCGVSLDVGGKKEYLIAGKAEGDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5987; S15987.
                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                              12
21
195
220
                                                                                                           98.6%;
ilarity 97.3%;
Conservative
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27
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39
39
154
172
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                                                                                                                                                                                                                                                                                                                                                                                                                           TIMP; 1.
                                                                                                                                                                                                                                                                                                               220
98
127
152
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                                                                                                                                                                                                                                                           201
193
164
                                                                                                                                                                                         24328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SHARMA R.R.,
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                                                                                                                                                                                            MW;
                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL.
                                                                                                                                                                                                                                                               BY SIMILARITY.
                                                                                                                    score 1620; DB 1;
pred. No. 0.00e+00;
5; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                         METALLOPROTEINASE INHIBITOR 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KISHI J.I.,
                                                                                                                                                                                                             -> E (IN
-> L (IN
-> H (IN
                                                                                                                                                                                            EBC62FFC CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ROCHELEAU H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ጅ
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N REF. 2).
N REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAYAKAWA T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TISSUE INHIBITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THE PRESENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SUCH AS COLLAGENASES)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GREENBERG A.H.,
                                                                                                                                                                 Length 220;
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                                                                                                                               Indels
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01-MAY-1991 (REL. 18, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
METALLOPROTEINASE INHIBITOR 2 PRECURSOR (TIMP-2)
METALLOPROTEINASES INHIBITOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIM2
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                                                                                                                                                                                                                                                               Query Match
Best Local S
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EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIMP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BOONE T.C., JOHNSOPROC. NATL. ACAD.
                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: HIGH WITH OTHER MEMBERS OF THE MALL, M32303, G163342; -- PIR; A32322; A25322. PIR; A35996; A35996. PIR; A34468; A3468; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 27-71.
MEDLINE; 90008914.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE: 86140235.
MURRAY J.B., ALLISON K., SUDHALTER J.,
BIOL. CHEM. 261:4154-4159(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-CARTILAGE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 27-71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLERCK Y. A., YEAN T.D., RATZKIN B.J., LU H.S., LANGLEY K.E.

BIOL. CHEM. 264:17445-17453(1282).

FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLI-
FUNCTION: THE ACTIVITY OF TIMP-2 IS DEPENDENT ON THE PRESENCE
FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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61 IYGNPIKRIQYEIKQIKMFKGPDQDIEFIYTAPAAAVCGVSLDIGGKKEYLIAGKAEGNG 120
                                                                     ARTIODACTYLA.
                                                                                                                                                                                                                                                                       Similarity
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ACAD. SCI. U.S.A. 87:2800-2804(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                               3
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220
98
127
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193
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56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                           E:
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BY SIMILARITY.
B
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pred. No. 0.00e+00;
12; Mismatches 6
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-> S (IN I
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                                                                                                                                                                                                                                                                                                                                                                                                                           CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIMP FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SUCH AS COLLAGENASES)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INHIBITOR
                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                 Length 220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAMMALIA
                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                  Gaps
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SULT
METALLOPROTEINASES-3) (MIG-5 PROTEIN).
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SILBIGER S.M., JACOBSEN V.L.,
GENE 141:293-297(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 NMHITLCDFIVPWDTLSATQKKSLNHRYQMGCECKITRCPMIPCYISSPDECLMMDWVTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. TISSUE-BREAST CARCINOMA; MEDLINE; 94228524.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE; 94308155.
                                                                                                                                                                                                                                                                                                                                                                                            URIA J.A., FERRANDO A.A., VELASCO G., FREIJE J.M., LOPEZ-OTIN C.;
CANCER RES. 54:2091-2094(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-KIDNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                          WILDE C.G., HAWKINS P.R., COLEMAN R.T., DELECEANE A.M., OKAMOTO P.M., ITO L.Y., DNA CELL BIOL. 13:711-718(1994).
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE; 95290091.
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE; 96404191.
                                                   MEDLINE; 94245184.
APTE S.S., MATTEI M.-G.,
GENOMICS 19:86-90(1994).
                                                                                                                                                                    SUBMITTED (SEP-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                       TOEHR H., ROOMP K., FELBOR U., WEBER B.H.F.; ENOME RES. 5:483-487(1995).
                                                                                                                               HAMMANI K.,
                                                                                                                SUBMITTED (MAY-1996)
                                                                                                                                    EQUENCE OF 42-211 FROM N.A. ISSUE-PLACENTA;
WEBER B.H.F., VOGT G., PRUETT R.C., NAT. GENET. 8:352-356(1994).
                                                                                                                                                                                                    EQUENCE FROM N.A.
                                                                                           EQUENCE OF 14-211 FROM N.A.
                                                                                                                                                                                                                                                                                                                                         CK M., BUERGER C., BRUESSELBACH S.,
BIOL. CHEM. 269:18953-18960(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PARIANTS SED CYS-191 AND CYS-204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     kmhitlcdfivpwdtlsttqkkslnhryqmgceckitrcpmipcyisspdeclwmdwvte
                                                                                                                                                                                         SSUE-RETINAL PIGMENT EPITHELIUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMAN
                                                                                  SSUE-PLACENTA;
                      95201800.
                                                                                                                     HENRIET P.M., SILBIGER S.M., I
MAY-1996) TO EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                 OLSEN B.R.;
                                                                                                                                 SILBIGER S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CUPPLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R.L.,
                 STOEHR H.,
                                                                                                                                                                                                                                                                                                                                                            LUCIBELLO F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B
                                                                                                                                                                                                                                                                                             LEVINE W.B.,
SCOTT R.W.,
                                                                                                                       DECLERCK Y.A.;
J DATA BANKS.
                     FELBOR U.;
                                                                                                                                                                                                                                                                                                                                                               MUELLER R.;
                                                                                                                                                                                                                                                                                                 SEILHAMER J.J.;
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VARIANT SED CYS-179.
WEDLINE; 96177683.
FELEOR U., STOEHR H., AMANN T., SCHOENHERR U., WEBER B.H.F.;
HUM. MOL. GENET. 4:2415-2416(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
-i- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
AND IRREVERSIBLY INACTIVATE THEM. MAY FORM PART OF A TISSUE-
AND IRREVERSIBLY INACTIVATE THEM. MAY FORM PART OF A TISSUE-
SPECIFIC ACUTE RESPONSE TO REMODELLING STIMULI.

SPECIFIC ACUTE RESPONSE TO REMODELLING SCIMULI.

-i- SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX.

-i- SUBCELLULAR LOCATION: EXTRACELLULAR MACULAR DISCORDER WITH DYSTROPHY (SPD), A RARE AUTOSOMAL DOMINANT MACULARIZATION AND ATROPHY OF CENTRAL VISION FROM SUBRETINAL INCOVASCULARIZATION AND ATROPHY OF CENTRAL VISION FROM SUBRETINAL INCOVASCULARIZATION AND ATROPHY OF CENTRAL VISION FROM SUBRETINAL MACULAR DISCIFORM DEGENERATION OF THE OCCULAR TISCUES. GENERALLY, MACULAR DISCIFORM DEGENERATION DEVELOPS IN THE PATIENTS EYE WITHIN 6 MONTHS TO 6 YEARS.

-I- SIMILARITY: HIGH WITH OTHER MEMBERS OF THE TIMP FAMILY.

-I- SIMILARITY: HIGH WITH OTHER MEMBERS OF THE TIMP FAMILY.
                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT SFD CYS-191.
MEDLINE; 96341630.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FELBOR U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               METALLOPROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /ARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                       Local Similarity 43.6%; pes 95; Conservation
114 YTGLCNEVERWDQLTLSQRKGLNYRYHLGCNCKIKSCYYLPCEVTSKNECLWTDMLSNEG 173
                                                   65
                                                                                                   60
                                                                                                                                                         7
                                                                                                                                                                         2 TPWLGLIVLLGSWSLGDWGAEACTCSPSHPQDAFCNSDIVIRAKVVGKKLVKEGP--FGT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S45317;
                                                pikriqyeikqikmfkg-pek-diefiytapssavcgvsldvggkkeyliagkaegdgkm 122
                                                                           -L--V-YTIKQMKMYRGETKMPHVQYIHTEASESLCGLKLEVN-KYQYLLTGRVY-DGKM 113
                                                                                                                                                      STOEHR H., AMANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; TIMP; 1. INHIBITOR;
                                                                                                                                                                                                                                                                                                                                                                   22 1
23 1
24145 MW;
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JOINED
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JOINED.
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BY SIMILARITY.
BY SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL; DISEASE MUTATION
                                                                                                                                                                                                                                                               Score 695; DB 1; L
pred. No. 1.17e-152;
56; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                              DW -> T (IN REF. 3).
AE -> R (IN REF. 8).
EA -> PR (IN REF. 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCHOENHERR U., APFELSTEDT-SYLLA E.,
                                                                                                                                                                                                                                                                                                                                                                           5FA15AAA CRC32;
                                                                                                                                                                                                                                                                                                                             Length 211;
                                                                                                                                                                                                                                                                                  Indels 12;
                                                                                                                                                                                                                                                                                        Gaps
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Best Local S
Matches 9
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P79121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
METALLOPROTEINASE INHIBITOR 3 PRECURSOR (TIMP-3) (TISSUE INHIBITOR
AC POT CO
                                                                                                                                                                               S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174 YPGYQSKHYACIRQKGGYCSWYRGWAPPDKSIINATDP 211
| |:| :|| :| |:||| || || ::: ||
| 183 inghqakffacikrsdyscawyrgaappkqefldiedp 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BOS TAURUS (BOVINE).
EUKARYOTA; METAZOA; CHORDATA;
EUTHERIA; ARTIODACTYLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIMP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA CELL BIOL. 15:1039-1048(1996).

-I- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
-I- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
-I- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
-I- FUNCTION: CONTROL OF A TISSUE-
SPECIFIC ACUTE RESPONSE TO REMODELING STIMULI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METALLOPROTEINASES-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 97138091.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX.
-1- SIMILARITY: HIGH WITH OTHER MEMBERS OF THE TIMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-PLACENTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METALLOPROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
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                       P39876;
01-FEB-1995 (REL.
01-FEB-1995 (REL.
01-OCT-1996 (REL.
                                                                                                                                                                                                                                                           METALLOPROTEINASE
                                                                                                     TIM3_MOUSE
                                                                                                                                                                                                  174 YPGYQSKHYACIRQKGGYCSWYRGWAPPDKSIINATDP
                                                                                                                                                                                                                                                                                                                                                                                          60
                                                                                                                                                                                     183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TPWLGLVVLLGSWSLGDWGAEACTCSPSHPQDAFCNSDIVIRAKVVGKKLLKEGP--FGT 59
                                                                                                                                                                                                                                                                                                                                                                                                                              tlriaigllila-tll-rpadacscspvhpqqafcnadvvirakavsekevdsgndiygn 64
                                                                                                                                                                                                                                                                                                                                                                                    -M--V-YTIKQMKMYRGFTKMPHVQYIHTEASESLCGLKLEVN-KYQYLLTGRVY-DGKM 113
                                                                                                                                                                                                                                                                                                                                              pikriqyeikqikmfkg-pek-diefiytapssavcgvsidvggkkeyliagkaegdgkm 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41.8%;
1 Similarity 43.1%;
94; Conservation
                                                                                                                                                                             145
150
163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INHIBITOR;
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                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118
143
192
155
184
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              INHIBITOR
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                   CREATED)
LAST EQUENCE UPDATE)
LAST ANNOTATION UPDATE)
LAST ANNOTATION (TIMP-3)
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METALLOPROTEINASE I
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred.
56; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 687; DB 1; Le pred. No. 1.83e-150; F. Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2AE2CB02 CRC32;
                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                             (TISSUE INHIBITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182
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METALLOPROTEINASES-3).
TIMP3 OR TIMP-3 OR SUN.
MUS MUSCULUS (MOUSE).
EUKARYOTA; METALOA; CHORI
                                                                                  MEDLINE;
LECO K.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE; 94179361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 94163596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-BALB/C; TIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUN Y., HEGAMYER G., COLBURN N. CANCER RES. 54:1139-1144(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-LUNG;
MEDLINE; 95036582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                 Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APTE S.S., HAYASHI K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEV. DYN. 200:177-197(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OLSEN B.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUN Y., HEGAMYER G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                      APTE S.S., OLSEN B.R., MURPHY G.;
J. BIOL. CHEM. 270:14313-14318(1995).
FUNCTION: COMPLEXES WITH METALLAPROTEINASES (SUCH PART OF AND IRREVERSIBLY INACTIVATE THEM. MAY FORM PART OF AND IRREVERSIBLY INACTIVATE THEM. MAY FORM PART OF SPECIFIC ACUTE RESPONSE TO REMODELING STIMULI SPECIFIC ACUTE RESPONSE TO REMODELING STIMULI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE; 95370262.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                         -I- SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX.
-I- TISSUE SPECIFICITY: HIGHEST LEVELS ARE FOUND IN KIDNEY, LT.
-I- TISSUE SPECIFICITY: HIGHEST LEVELS ARE FOUND IN FOLLOWED BY OVARY AND UTBRUS. LOW LEVELS ARE FOUND INDUCTION: HIGHLY INDUCED BY PHORBOL ESTER (PMA), EGF AND INDUCTION: HIGHLY INDUCED BY PHORBOL ESTER (PMA) TRANSFORMING GROWTH FACTOR BETA 1. ALSO INDUCED BY DEXAMET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 95301511.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-129,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COLBURN N.H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (EDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BIOL. CHEM.
                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                              -1- SIMILARITY: HIGH WITH OTHER MEMBERS
                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                        EMBL;
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                                                                                                DISULFID DISULFID
                                                                                                                                                                                                                                         PIR;
                                                                                                                                                                                                                                                   PIR;
                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       К.J.,
                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                            MGD;
                                                                                                                                                                                                  METALLOPROTEASE
                                                                                                                                                                           CHAIN
                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                   L27424; G439882;
Z30970; E264421;
L19622; G438811;
U26437; G1167534;
                                                                                                                                                                                                                          MGI:98754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RODENTIA.
TPWLGLVVLLSCWSLGHWGAEACTCSPSHPQDAFCNSDIVIRAKVVGKKLVKEGP--FGT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KHOKHA R., PAVLOFF N., HAWKES
HEM. 269:9352-9360(1994).
                                      Similarity
94; Conserv
                                                                                                                                                                                                                 PS00288;
                                                                                                                                                                                                                                                                      33; G1167534; JOINED.
34; G1167534; JOINED.
35; G1167534; JOINED.
36; G1167534; JOINED.
                                                                                                                                                                                                                                                                    5; G1167534;
6; G1167534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-SKIN, AND LUNG
                                                                                        24
24
26
36
145
150
150
                                                                                                                                                                                                                                            S43052
                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHORDATA;
                                                                                                                                                                                                      INHIBITOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COLBURN N.H.;
                                                                                                                                                                                                                       TIMP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KIM H., SITHANANDAM
                                                                                                                                            91
118
143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SELDIN M.F.,
                                                        41.8%;
43.1%;
                                                                                            24182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERTEBRATA;
                                                                                                        METALLOPROTEINASE INHIBITOR 3.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                歪
                                                                                                                                                                                                            SIGNAL
                                               Score
Pred.
56; N
                                                                                                                                                                                                 POTENTIAL
                                                                                                 CCB6E436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MATTEI M.-G., HAYASHI M.,
                                                   a 686; DB 1; Leu
No. 3.44e-150;
No. 56;
                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.
.
                                                                                                    CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LI H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDWARDS
                                                                          Length 211;
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                                                                                                                                                                                                                                                                                                                                                                                             BY DEXAMETHASONE
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                                                        Indels
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Best Local S
Matches 9
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DISULFID
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01-AUG-1992 (REL. 24, LAST SEQUENCE UPDATE)
01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
METALLOPROTEINASE INHIBITOR 3 PRECUSOR (TIMP-3) (TISSUE INHIB
METALLOPROTEINASE INHIBITOR 3 PROTEIN OF EXTRACELLULAR MATRIX).
                                                                                                                                                                                                      DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                                                                           STASKUS P.W., MASIARZ F.R., PALLANCK L.J., HAWKES S.P.;
J. BIOL. CHEM. 266:449-454(1991).

-I- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS AND IRREVERSIBLY INACTIVATE THEM. MAY FORM PART OF A SPECIFIC ACUTE RESPONSE TO REMODELING STIMULI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-EMBRYONIC
MEDLINE; 92381050
PAVLOFF N., STASK
                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-FIBROBLAST;
MEDLINE; 91093162.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GALLIFORMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EUKARYOTA; METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GALLUS GALLUS
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                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                          METALLOPROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 25-53.
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               134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174 YPGYQSKHYACIRQKGGYCSWYRGWAPPDKSISNATDP 211
                                                                76
                                                                                        24
                                                                                                              22 AEACTCVPIHPQDAFCNSDIVIRAKVVGKKLMKDGP--FGT-M-R--YTVKQMKMYRGFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BIOL. CHEM.
                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: EXTRACELLULAR SIMILARITY: HIGH WITH OTHER MEMBERS
                                                                                                                                                                                                                                                                                                                                 A39043; A39043
A43429; A43429
KGLNHRYHLGCGCKIRPCYYLPCFATSKNECIWTDMLSNFGHSGHQAKHYACIQRVEGYC
                                   ek-dieflytapssavcgvsldvggkkeyllagkaegdgkmhitlcdfivpwdtlsttqk 141
                                                                                    adacscspvhpqqafcnadvvirakavsekevdsgndiygnpikriqyeikqikmfkg-p
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                                                            IMPHVQYIYTEASESICGVKLEVN-KYQYLITGRVY-EGKVYTGLCNWYEKWDRLTLSQR 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pikriqyeikqikmfkg-pek-diefiytapssavcgvsldvggkkeyliagkaegdgkm
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                                                                                                  M94531; G211902;
                                                                                                                                       Similarity 45.2%;
90; Conservative
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PS00288; T
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212
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M. 267:17321-17326(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CHICKEN).
                                                                                                                                                                                                   E INHIBITOR;
1 24
5 212
6 92
7 119
7 114
6 193
6 193
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4 185
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                                                                                                                                                                                                                                                                                                                      TIMP;
                                                                                                                                                    41.8%;
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                                                                                                                                                                                       24504 MW;
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                                                                                                                                                                                                                                                                                                        SIGNAL.
                                                                                                                                                                                                  METALLOPROTEINASE 1
BY SIMILARITY.
                                                                                                                                                    Score 686; DB 1; I
Pred. No. 3.44e-150;
                                                                                                                                         49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                        Mismatches
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                                                                                                                                        50;
                                                                                                                                                              Length 212;
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                                                                                                                                       Indels
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                                                                                                                                     Gaps
              193
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Best Local
                                                                                                TIM1_PAPCY
P49061;
01-FEB-1996
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01-FEB-1996
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TIMP1.
PAPIO CYNOCEPHALUS (YELLOW BABOON)
EUKARYOTA; METAZOA; CHORDATA; VERT
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RATTUS NORVEGICUS (RAT) EUKARYOTA; METAZOA; CHC
                                                                             METALLOPROTEINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION:
-!- SIMILARITY: HIGH WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WU I., MOSES M.A.;
SUBMITTED (MAY-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METALLOPROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIMP3 OR TIMP-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METALLOPROTEINASES - 3).
                                                                                                                                                                                                                                                       183 inghqakffacikrsdgscawyrgaappkqefldiedp
                                                                                                                                                                                                                                                                                                 174 YPGYQSKHYACIRQKGGYCSWYRGWAPPDKSISNATDP 211
                                                                                                                                                                                                                                                                                                                                               123
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                                                                                                                                                                                                                                                                                                                                                             114 YTGLCNEVERWDHLTLSQRKGLNYRYHLGCNCKIKSCYYLPCFVTSKKECLWTDMLSNFG
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                                                                                                                                                                                                                                                                                                                                  tlrlalglllla-tl-lrpadacscspvhpqqafcnadvvirakavsekevdsgndiygn 64
                                                                                                                                                                                                                                                                                                                                                                                                                        pikriqyeikqikmfkg-pek-diefiytapssavcgvsldvggkkeyliagkaegdgkm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                -L--V-YTIKQMKMYRGFSKMPHVQYIHTEASESLCGLKLEVN-KYQYLLTGRVY-EGKM 113
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93; Conser
                                                                                                  (REL.
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llarity 42.7%;
Conservative
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24226 MW;
                                                                                                                                                                                STANDARD;
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                                                                                   33, CREATED)
33, LAST SEQUENCE UPDATE)
33, LAST ANNOTATION UPDATE)
                                                                             INHIBITOR 1
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                                                                                                                                                                                                                                                                                EXTRACELLULAR OTHER MEMBERS
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Pred. No. 1.52e-148;
56; Mismatches 57;
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                  VERTEBRATA; TETRAPODA;
                                                                             PRECURSOR
                                                                                                                                                                                PRT;
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OF THE TIMP
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                  MAMMALIA;
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SEQUENCE FROM N.A.

MEDLINE; 85240567.

GASSON J.C., GOLDE D.W., F

KAUFMAN R.J., WONG G.G., 1

ORR E.C., CLARK S.C.;
                                                      SEQUENCE FROM N.A.
MEDLINE: 86040463.
DOCHERTY A.J.P., LYONS A.,
HARRIS T.J.R., MURPHY G., F
NATURE 318:66-69(1985).
                                                                                                                          TIM1_HUMAN
P01033; Q14252;
21-JUL-1986 (RE
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SEQUENCE FROM |
TISSUE-AORTA;
                                                                                                                   TIMP1 OR TIMP.
HOMO SAPIENS (HUMAN)
EUKARYOTA; METAZOA; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE: 96011646.
FOROUGH R., NIKKARI S.T., HASENSTAB D.,
GENE 163:267-271(1995).
                                                                                                           EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLYCOPROTEIN; METALLOPROTEASE INHIBITOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE
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                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: COMPLEXES WITH METALLOPROTEINASES AND IRREVERSIBLY INACTIVATE THEM.
PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON
                                                                                                                                                                                                                                                                                                                                                            LASGILLLLMLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTT-LYQRYEIKM 65
                                                                                                                                                                                                                                                  qakffacikrsdgscaw
                                                                                                                                                                                                                                                                    QSRHLACLPREPGLCTW 199
                                                                                                                                                                                                                                                                                      dfivpwdtlsttqkkslnhryqmgce-ckitrcpmipcyisspdeclwmdwvtekningh 186
                                                                                                                                                                                                                                                                                                        SFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEKGF
                                                                                                                                                                                                                                                                                                                        iqyeikqikmfkgpekdiefiytapssavcgvsldvggkke-yliagkaegdgkmhitlc 127
                                                                                                                                                                                                                                                                                                                                          TK-MYKGFQAL-GDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQ-DGLLHITTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L37295; G561546;
E; PS00288; TIMP
                                                                                                                                                                                                                                                                                                                                                                                                Similarity
81; Conser
                                                                                                            PRIMATES.
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larity 41.1%;
Conservative
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23213
                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIGH WITH
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                                                                                                                     CHORDATA;
                                                                                                                                                                                                                                                 203
                                                                       ` <del>?</del>
          KAUFMAN
TEMPLE P
                                                                                                                                                                                                                                                                                                                                                                                                                                     ₹
:
                                                               REYNOLDS J.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER MEMBERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.

METALLOPROTEINASE INHIBITOR 1.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                               Score 521; DB 1; L
Pred. No. 2.28e-105;
39; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENT IAL
                                                                                                                     VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                    14EFBDAE CRC32;
          P.A.,
                S.E.,
                                                                                                                                                                                                              207
          WESTBROOK C.A.,
LEARY A.C., BROW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEA H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ERYTHROCYTE MATURATION;
                                                                                                                     TETRAPODA; MAMMALIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THE
                                                                        E.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                Length 207;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SUCH AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLOWES A.W.;
                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRESENCE
                                                                         STEPHENS
          HEWICK R.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COLLAGENASES)
                                                                                                                                                                                                                                                                                                                                                                                                7;
                                                                    P.E.,
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                        182
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O'SHEA M., WILLENBRUCA...
FREEDMAN R.B., REYNOLDS J.J., DOCHERTY A....
FREEDMAN R.B., REYNOLDS J.J., DOCHERTY A....

BIOCHEMISTRY 31:10146-10152(1992).

-I- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
-I- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
-I- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
-I- FUNCTION: SUCH AS COLLAGENASES (SUCH AS COLLAGENASES)
-I- FUNCTION: SUCH AS COLLAGEN
                                                                                                      EMBL;
PIR;
PIR;
                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                         DISULFIDE BUND.
-I- SIMILARITY: HIGH WITH
EMBL; X03124; G37183; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE: 94123576.
OPBROEK A., KENNEY M.C., BROWN D
CURR. EYE RES. 12:877-883(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 86205964.

CARMICHAEL D.F., SOMMER A.,
WELGUS H.G., STRICKLIN G.P.
                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=SYNOVIAL FL
MEDLINE; 92111776.
OSTHUES A., KNAUEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WILLIAMSON R.A., MARTSON F.A.C MORRIS H.R., CARNE A.F., SMITH BIOCHEM. J. 268:267-274(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MATSUDA T., KOHNO K., KUWANO
SUBMITTED (JUL-1992) TO EMBL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 42-207 FROM N.A. MATSUDA T., KOHNO K., KUWANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RAPP G., FRE SCHEIT K.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBMITTED (SEP-1995) TO EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WELGUS H.G., STRICKLIN G.P.;
PROC. NATL. ACAD. SCI. U.S.A. 83:2407-2411(1986).
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[3]
                                                                                                                                                                                                                                                                                                                                                      -! - PTM: THE ACTIVITY OF TIMP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HARDCASTLE A.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-40 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-OVARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQUENCE OF 24-38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , KNAUEPER V., OB
296:16-20(1992)
                                                                                                                                                                                                                                                  G182483; -.
G31189; -.
288; TIMP; 1.
METALLOPROTEASE INHIBITOR; ERYTHROCYTE MATURATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9:479-485(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FLUID;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J., KLAUDINY J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UWANO M.;
EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIBES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OBERHOFF
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SMITH B.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BROWN D.;
                                                                                                                                                                                                                                                                                                                OTHER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REINKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MUCHA J.,
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S T.J.R.,
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FREEDMAN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARTWRIGHT T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H.;
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01-FEB-1991
01-NOV-1995
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P20614;
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SIGNAL
CHAIN
                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                            HOROWITZ S., DAFNI N., SHAPIRO D.L., QUIBLE D.J.;
J. BIOL. CHEM. 264:7092-7095(1989).
-!- FUNCTION: COMPLEXES WITH METALLO!
                                                                                                                                                                                                PROSITE; PS00288;
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE; 89214135.
                                                                                                                                                                                                                                                                                                                                                                                                                              EUKARYOTA; METAZOA; C
EUTHERIA; LAGOMORPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                            ORYCTOLAGUS CUNICULUS (RABBIT EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                  PIR; A33350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 METALLOPROTEINASE
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                                                                                                                                                                                                                                                                              AND IRREVERSIBLY INACTIVATE PTM: THE ACTIVITY OF TIMP-1
                                                                                                                                                                                                                                                                DISULFIDE BONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qakffacikrsdgscaw
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            iqyeikqikmfkgpekdiefiytapssavcgvsldvggkke-yliagkaegdgkmhitlc
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81; Conse
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                                                                                                                                                                                  METALLOPROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                 TIMP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17, CREATED)
17, LAST SEQUENCE UPDATE)
32, LAST ANNOTATION UPDATE)
INHIBITOR 1 PRECURSOR (TIMP-1).
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                                                                                                                                                                                                                                               OTHER MEMBERS OF
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METALLOPROTEINASE I
BY SIMILARITY.
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BY SIMILARITY.
POTENTIAL.
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Pred. No. 2.28e-105;
39; Mismatches 70;
                                                                                                                                                                                                                                                                                                         METALLOPROTEINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                   VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METALLOPROTEINASE INHIBITOR
                                                                                                                                                                                INHIBITOR;
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-> P (IN REF. 7).
8B7E3B4E CRC32;
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IS DEPENDENT ON
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                                                                                                                                                                               ERYTHROCYTE
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                                                                                                                                                                                                                                                                                                                                                              B.A.,
                                                                                                                                                                                                                                              THE TIMP
                                                                                                                                 INHIBITOR
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                                                                                                                                                                                                                                                                                                            (SUCH AS COLLAGENASES)
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                                                                                                                                                                                                                                               FAMILY
                                                                                                                                                                                                                                                                              PRESENCE
                                                                                                                                                                                MATURATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207;
                                                                                                                                                                                                                                                                                                                                                              R.H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1991
01-FEB-1991
01-FEB-1996
DISULFID
DISULFID
DISULFID
CARBOHYD
CARBOHYD
SEQUENCE
                                                      DISULFID DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                                                      BOS TAURUS EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                TIM1_BOVIN P20414;
                                                                                                                              EMBL; M60073; G163761; -.
EMBL; S70841; G546974; -.
PIR; A35685; A35685.
PIR; B34468; B34468
                                                                                                                                                                                      -i- FUNCTION: COMPLEXES WITH METALLOPROTEINASES AND IRREVERSIBLY INACTIVATE THEM.
-i- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE; 94257757. SATOH T., KOBAYASH
                                                                                                              PROSITE; PS00
GLYCOPROTEIN;
                                                                                                                                                                  DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE; 90365711.
FREUDENSTEIN J., WAGNER
BIOCHEM. BIOPHYS. RES. (
                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1991 (REL. 17, CREATED)
01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
METALLOPROTEINASE INHIBITOR 1 PRECURSOR (TIMP-1) (EMBRYOGENIN-1) (EG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                   CHAIN
                                                                                            SIGNAL
                                                                                                      SIGNAL.
                                                                                                                                                                                                                                     MEDLINE; 90008914
                                                                                                                                                                                                                                              PRELIMINARY SEQUENCE OF 24-69
                                                                                                                                                                                                                                                                 BIOL. REPROD.
                                                                                                                                                                                                                                                                                                                                                                                           TIMP1.
                                                                                                                                                                                                                 DE CLERCK Y.A., YEAN T.D., RATZKIN F. BIOL. CHEM. 264:17445-17453(1989)
                                                                                                                                                                                                                                                                                                                                                              EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182
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                                                                                                                                                                                                                                                                          KOBAYASHI K.,
                                                                                                                                                                                                                                                                                                                                                             ; METAZOA; CHO
ARTIODACTYLA.
                                                                                                                                                                                                                                                                                                                                                               (BOVINE).
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                   Conservative
                                                                                                                                                                                                                                                                AYASHI K., YAMASHITA
50:835-844(1994).
                                                                                                              METALLOPROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                        TIMP;
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      METALLOPROTEINASE I
BY SIMILARITY.
POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 518; DB 1; I
Pred. No. 1.46e-104;
39; Mismatches 71;
                                                                                                              INHIBITOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                      VERTEBRATA; TETRAPODA;
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                                                                                                                                                                                                                                                                         s.,
                                                                                                                                                                                                                           B.J.,
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                                                                                                                                                                                                                                                                          KIKUCHI M.,
 CRC32;
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                                                                                                             ERYTHROCYTE
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                                                                                                                                                                                                                           LANGLEY K.E.;
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                                                                                                                                                                                                                                                                         SENDAI Y.,
                                                                                                                                                                                       PRESENCE
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                                                                                                              MATURATION;
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                                                                                                                                                                                                                                                                                                                         SCHEIT
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                                                                                                                                                                                                                                                                                                                         K.H.;
                                                                                                                                                                                                                                                                          HOSHI H.;
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TRESULATION OF THE PROPERTY OF
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Best Local S
Matches 7
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Best Local Similarity
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P50122;
                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMITH G.W., GOETZ T.L., ANTHONY ENDOCRINOLOGY 134:344-352(1994)
-I- FUNCTION: COMPLEXES WITH ME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
METALLOPROTEINASE INHIBITOR 1 PRECURSOR (TIMP-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OVIS ARIES
                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLYCOPROTEIN; METALLOPROTEASE INHIBITOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-CORPORA LUTEA; MEDLINE; 94102210.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EUKARYOTA;
    126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                    eikqikmfkgpekdiefiytapssavcgvsldvggkke-yliagkaegdgkmhitlcdfi 130
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                                                                        MFKGFSALRDAP-DIRFIYTPAMESVCGYFHRSQNRSEEFLIAGQL-SNGHLHITTCSFV 125
                                                                                                                   gllllatllrpadacscspvhpqqafcnadvvirakavsekevdsgndiygn-pikriqy
                                                                                                                                                             GILLLWLTAPSRACTCVPPHPQTAFCNSEVVIRAKFVGTAEVNE-TALYQRYEIKMTK- 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QSRHLACLPREPGLCTW 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S67450; G456990;
                                                                                                                                                                                                      Similarity 76; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS00288; TIMP; 1
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                                                                                                                                            31.5%;
                                                                                                                                                                                                                         31.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTHONY R.V., SMITH M.F.;
                                                                                                                                        Œ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER
                                                                                                                                                                                                                                                                                                                                              METALLOPROTEINASE I
BY SIMILARITY.
                                                                                                                                                                                                      Score 515; DB 1; Le
Pred. No. 9.28e-104;
42; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 517; DB 1; L
Pred. No. 2.70e-104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METALLOPROTEINASES (SUCH AS COLLAGENASES)
                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY
                                                                                                                                                                                                                                                                                                                               POTENTIAL.
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Matches 7
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P30120;
01-APR-1993 (REL.:
01-NOV-1995 (REL.:
01-OCT-1996 (REL.:
                                                                                                     CONFLICT
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EMBL; L31883; G1161234; -.
EMBL; U16022; G562119; ALT_SEQ
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MEDLINE; 95011636.
OKADA A., GARNIER J.M.,
                                                                                                                                                                                                                                                                                  PIR;
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                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                           GLYCOPROTEIN; METALLOPROTEASE INHIBITOR; ERYTHROCYTE MATURATION;
                                                                                                                                                                                                                                                                                                                             DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                     - I- PTM: THE ACTIVITY OF TIMP-1
                                                                                                                                                                                                                                                                                                                                                                           ROSWIT W.T., MCCOURT D.W., PARTRIDGE N.C., JEFFREY J.J.;
ARCH. BIOCHEM. BIOPHYS. 292:402-410(1992).
-I- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 24-45.
MEDLINE; 92117648.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GIBBONS K.L., O'GRADY R.L., PIPER A.A.;
SUBMITTED (JAN-1996) TO EMBL/GENBANK/DDBJ
                                                                                                                                                                          DISULFID
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BOUJRAD N., GA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENE 147:301-302(1994).
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 10
            7 LASGILLLISLIASSKACSCAPTHPQTAFCNSDLVIRAKFMGSPEI-IETTLYQRYEIKM 65
vpwdtlsttqkkslnhryqmgce-ckitrcpmipcyisspdeclwmdwvtekninghqak
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32, LAST SEQUENCE UPDATE)
34, LAST ANNOTATION UPDAT
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                                                                                          23793 MW;
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                                          Score 508; DB 1; I
Pred. No. 6.98e-102;
39; Mismatches 78;
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Search	Ϋ́	망	γ	В	Qy	В	
0	187	183	128	123	69	66	
Search completed: Mon May 4 14:49:58 1998	187 qakffac1krsdyscaw-yrgaa 208	183 QSDHFACLPRNPDLCTWQYLGVS 205	128 dfivpwdtlsttqkkslnhryqmgce-ckitrcpmipcyisspdeclwmdwvtekningh 186	123 SFLVPWHNLSPAQQKAFVKTYSAGCGVCTVFPCSAIPCKLESDSHCLWTDQILMGSEKGY 182	69 iqyeikqikmfkgpekdiefiytapssavcg-vsldvggkkeyliagkaegdgkmhitlc 127	66 TK-MLKGFDAV-GNATGFRFAYTPAMESICGYVHKSQNRSEEFLIAGRIR-NGNIHITAC 122	

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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
on: Mon May 4 14:42:49 1998; MasPar time 144.53 Seconds

on: Mon May 4 14:42:49 1998; MasPar time 144.53 Seconds 824.777 Million cell updates/sec

Title: >Q06584
Description: (1-1033) from n-geneseq.seq
Perfect Score: 1033
N.A. Sequence: 1 attccggccgccgtccccc.....

1 attccggcccgccgtccccc.....acactcatccccggaattc 1033 taaggccgggcggcaggggg.....ttgtgagtaggggccttaag

Scoring table: TABLE default
Gap 6

Comp:

Nmatch STD : Dbase 0; Query 0

Searched: 159651 seqs, 57698962 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

n-geneseq30

l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7

8:part8 9:part9 10:part10 11:part11 12:part12 13:part13

14:part14 15:part15 16:part16 17:part17 18:part18

19:part19 20:part20 21:part21 22:part22 23:part23

24:part24 25:part25 26:part26 27:part27 28:part28

29:part29 30:part30 31:part31 32:part32 33:part33

tistics: Mean 9.064; Variance 6.093; scale 1.488

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES .

Result No.	.t Score	Query Match	ry ch Length	yth DB	ID .	Description	Pred. No.
	1 1033		:	1033 1	Q06584	Sequence encoding hum	0.00e+00
	2 1031	31 99.8		1033 13	Q73088	Human metalloproteina	0.00e+00
	3 70			730 1	Q05940	Complete sequence of	0.00e+00
	4 60			340 1	Q05938	TIMP-2 metalloprotein	0.00e+00
	5			832 1	Q05939	TIMP-2 metalloprotein	0.00e+00
	6				T64341	Human small tissue in	0.00e+00
	7 59)45 1	Q06583	Sequence encoding bov	0.00e+00
	8 59				Q73087	Bovine metalloprotein	0.00e+00
	9 28				T26262	Human gene signature	1.22e-157
	10				T34433	Tissue inhibitor of m	7.46e-45
	I 1			75 32	T80986	Tissue inhibitor of m	1.15e-43
0	2)47 2	Q10572	Human Natriuretic Pep	3.92e-26
	<u>ت</u>)47 2	010572	Human Natriuretic Pep	7.50e-24
	[4			320 16	T02361	TIMP-3 clone Timp3HCM	1.38e-21
	5			963 16	T02360	TIMP-3 DNA clone Timp	1.38e-21
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Human defensin 1 anti Human leukotriene C4	Generic DNA sequence	Generic DNA sequence	Generic DNA sequence	ω H	Generic DNA sequence			^	endothelin-1		metallopro	neutrophil	substituted E.c	Human interleukin 8 a	Oligonucleotide probe	Human intercellular a	Chicken tissue inhibi	Substance P receptor	RANTES antise	Human IL6 antisense o	Ä.				Synthetic fragment of	TIMP-3 metalloprotein	Human tissue inhibito	TIME 3 DWA CLONE TIME
5.24e-07 5.24e-07	5.24e-07	5.24e-07	.24e	.63e	•	. 01e	.53e-	. 53e	4.64e-09	4.64e-09	4.64e-09	٠	1.40e-09	1.40e-09		1.25e-10	.09e-	.09e-	.09e-	.69e-	.09e	.09e-	.17e-	4.03e-17	.84e-2	.38e-	.38e-	2e-7

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18-MAY-1990;
19-MAY-1989;
29-MAR-1990;
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New metallo:proteinase inhibitor, analogues and DNA - for treating tumour cell dissemination, rheumatoid arthritis large-scale recombinant inhibitor produ.

Claim 12; Fig 2; 65pp; English.

Q73088 encodes R62769 human metalloproteinase inhibitor may be used to inhibit tumour cell dissemination and for rheumatoid arthritis, dystrophic epidermolysis bullosa, and osteoporosis. The DNA may be used to detect MI gene sequence 1033 BP; 215 A; 360 C; 305 G; 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human metalloproteinase inhibitor cDNA.

Metalloproteinase inhibitor; tumour cell dissen

rheumatoid arthritis; dystrophic epidermolysis

emphysema; osteoporosis; MI gene disorders; ss.
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Langley KE;
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**17-JUL-1989; US-380631.

18-AUG-1989; US-395453.

13-MAR-1990; US-494796.

(USSH) NAT INST OF HEALTH.

Stetler-Sevenson WG, Liott-
WEI: 3G-790697738.

**PSDB; R06800

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New matrix metallo-proteinase inhibitor resulting from matrix metallo-proteinase diagnosis, detection and purific. Disclosure; Fig 7; 54pp; English.
                                                                                                                                                                                                                                                                                                          Complete sequence of huma matrix metalloproteinase
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Q05940;
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Q05938

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Q05938; 16-JAN-1991 (first entry) TIMP-2 metalloproteinase in matrix metalloproteinase in Synthetic.

inhibitor; inhibitor encoding inhibitor; TIMP-2;

pSS15;

pSS15.

(first entry)

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See also Q05937, R06746-R06750, R06894-R06895 and Q05938-Q05939. Sequence 730 BP; 189 A; 209 C; 201 G; 131 T;
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Pred. No. 0.00e+00;
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PS Disclosure; Fig 6A; 54pp; English.

CC TIMP-2 was isolated from human melanoma cell-conditioned media and the amino acid sequence determined. A probe was synthesised based upon the protein sequence information. It was used to screen comparison of the protein sequence information. It was used to screen electrical actions and the protein sequence of 750,000 plaques screened. CC positives were identified from a total of 750,000 plaques screened. CC Further analysis and screening with additional probes eliminated to encode CSC-21K (=TIMP-2), a novel metalloproteinase inhibitor.

CC See also US331407 and w09010228.

CC See also US337, R06746-R06750, R06894-R06895 and Q05939-Q05940.
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(USSH) NAT INST OF HEALTH.
Stetler-Sevenson WG, Liotta
WPI; 90-290097/38.
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To diagnosis, detection and purificm.

So Disclosure; Fig 6B; 54pp; English.

CITMP-2 was isolated from human melanoma cell-conditioned media and control of the amino acid sequence determined. A probe was synthesised control of the protein sequence information. It was used to screen can based upon the protein sequence information. It was used to screen can be a sequence determined from human melanoma cells. 239 contitives were identified from a total of 750,000 plaques screened. CC Further analysis and screening with additional probes eliminated control of clones (pSSI5 and pSSI8). Both were sequenced and found concode CSC-2IK (-TIMP-2), a novel metalloproteinase inhibitor. CC see also USC317407 and w09010228.

CC See also USC317407 and w09010228.

CC See also USC337, R06746-R06750, R06894-R06895, Q05938 and Q05940.
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21-MAR-1989; US-386334.
17-JUL-1989; US-380431.
18-AUG-1989; US-395453.
18-AWR-1990; US-494796.
(USSH) NAT INST OF HEALTH.
Stetler-Sevenson WG, Liotta L#
WPI; 90-290097/38.
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gcacatcaccctctgtgacttcatcgtgccctgggacaccctgagcacca
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The present sequence is that of the human small tissue inhibitor metalloprotease 2 (TIMP2) DNA. Expression of this sequence is negatively correlated with brain tumour malignancy, i.e. relative expression levels are: normal brain tissue > astrocytoma > anaplastic astrocytoma > glioblastoma. By determining the level of TIMP 2 expression in human brain tissue, the malignancy of cerebit tumours can be evaluated.

Sequence 671 BP; 177 A; 184 C; 196 G; 114 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            the
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22-JUN-1995; JP-156307.
(EISA) EISAI CO LTD.
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human small tissue inhibitor metallo:protease 2 gene - use detection of cancer, and to inspect malignancy of cerebral
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                                       cgttggaggaaagaaggaatatctcattgcaggaaaggccgaggggggacggcaagatgca
catcaccctctgtgacttcatcgtgccctgggacaccctgagcaccacccagaagaagag
                           cgttggaggaaagaaggaatatctcattgcaggaaaggccgagggggggcggcaagatgca
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l Similarity 100.0%;
629; Conservative
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Query Match
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Matches 70
                                                                           Claim 12; Fig 1; 63pp; English.
Sequence may be used to transform a procaryotic or eukaryotic expression system to give a product with all the biological properties of naturally occuring metalloproteinase inhibitor. The product has therapuetic use in inhibiting tumour dissemination during chemotherapy and radiation therapy, impurged bone marrow ce harvesting etc. The inhibitor may also be useful in encapsulating tumours aiding clean excision, and in treatment of enphysema, Page disease, osteoporosis, scleroderma and bedsores.
The gene product also has application in autoimmune disorders eg. The onessed of arthritis and multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                       mat_peptide
/*tag= b
EP-398753-A.
                                                                                                                                                                                                                                   New metallo-proteinase inhibitor polypeptide(s) - and DNA encoding them, for treatment of tumour cell dissemination rheumatoid arthritis
                                                    See also Q06584.
Sequence 1045 BP;
                                                                                                                                                                                                                                                                                          Langley KE, Boone : WPI; 90-350481/47.
                                                                                                                                                                                                                                                                                                    (AMGE-) AMGEN INC.
(CHIL-) CHILDREN'S HOSPITAL OF
Tangley KE, Boone TC, DeClerck
                                                                                                                                                                                                                                                                                                                                                  19-MAY-1989;
29-MAR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus.
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US-355027.
US-501904.
58.0%;
llarity 89.6%;
Conservative
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Pred. No. 0.00e+00;
0; Mismatches 77;
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EP-623676-A.
09-NOV-1994.
18-MAY-1990;
                                                        emphysema;
Bos taurus.
Key
                                                                     13-JUL-1995 (first entry)
Bovine metalloproteinase inhibitor; tumour cell dissemination;
Metalloproteinase inhibitor; tumour cell dissemination;
rheumatoid arthritis; dystrophic epidermolysis bullosa;
emphysema; osteoporosis; MI gene disorders; ss.
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                                                Location/Qualifiers 289..951
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Best Local Similarity 89.6%;
Matches 706; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New metallo:proteinase inhibitor, analogues and DNA - for treating tumour cell dissemination, rheumatoid arthritis and for large-scale recombinant inhibitor prodn.

Claim 12; Fig 1; 65pp; English.

Q73087 encodes R62768 bovine metalloproteinase inhibitor (MI), it may be used to inhibit tumour cell dissemination and for treating rheumatoid arthritis, dystrophic epidermolysis bullosa, emphysema and osteoporosis. The DNA may be used to detect MI gene disorders. Sequence 1045 BP; 219 A; 350 C; 311 G; 165 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-MAY-1989; US-355027.
29-MAR-1990; US-501904.
(AMGE-) AMGEN INC.
(CHIL-) CHILDRENS HOSPITAL
Boone TC, Declerck YA, La
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                                    agatcaagcagataaagatgttcaagggacctgatcaggaccatagagtttatctacacag
                                                                                          cctgcatcaagagaagcgacggctcctgcgcctggtaccgcgggagcagcagcacccccaagc
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       -acagtgtccaagagttcagactggtccagctccgacatcccttcctggacacagca
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Langley KE;
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Pred. No. 0.0
0; Mismatcl
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.+~hes 77;
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Matches 28
T34433 standa
T34433;
T34433;
09-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a CDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.

Sequence 302 BP; 75 A; 96 C; 75 G; 53 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, CDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene signature; messenger RNA; mRNA; relative human; cloning; mapping; non-biased library;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying gene signatures in 3'-directed human cDNA library -
for diagnosis of abnormal cell function, by preparing cDNA that
reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matsubara K, Okubo K;
WPI; 95-206931/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cell typing; abnormal Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human gene signature
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12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
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l Similarity 99.0%;
288; Conservati
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Pred. No. 1.22e-157;
0; Mismatches 3;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A full-length cDNA clone (T34433) codes for human tissue inhibitor of metalloproteinase-4 (TIMP-4) (R98265), which was identified as a novel member of the TIMP family. The cDNA clone was obtd. from a cDNA ilbrary derived from an early stage human brain. It can be used for prodn. of recombinant TIMP-4, using e.g. Escherichia coli, COS or insect cell hosts. It can also be used in gene therapy, or to design probes for use in diagnosis of a disease, or a susceptibility to a disease, related to a mutation in the human TIMP-4 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding human tissue inhibitor of metalloproteinase-4 (TIMP-4) useful to treat, e.g. cancer, arthritic diseases, bone resorption
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME
Greene JM, Rosen CA;
WPI; 96-300644/30.
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13-DEC-1994; WO-U14498
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                                                                             453 ctaccatctgaactgtggctgccaaatcaccacctgctacacagtaccctgtaccatctc
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                                                                                                                                       273 gtatatotatacgcottttgactottccctctgtggtgtgaaactagaagccaacagcca
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                  ggcccctaacgagtgcctctggacagactggctgttggaacgaaagctctatggttacca
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llarity 61.9%;
Conservative
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1..87
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of metalloproteinase-4; TIMP-4; cancer;
Paget disease; gene therapy; diagnosis;
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Pred. No. 7.46e-45;
0; Mismatches 232
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Matches 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence encodes a tissue inhibitor of metalloproteinases designated TIMP-4. This clone was identified with Incyte Clone No. 589345. TIMP-4 can be used to treat disorders associated with excessive metalloprotease expression, e.g. tumour metastasis, angiogenesis and growth, osteo-arthritis, osteoporosis, pulmonary emphysema, periodontal disease and rheumatoid arthritis, and for contraception. TIMP-4 cDNA can be used for gene therapy of such disorders and in diagnostic assays for TIMP-4 mRNA in cells and tissues. Oligonucleotide fragments of the TIMP-4 cDNA and antagonists or inhibitors of TIMP-4 can be used to treat disorders and antagonists or inhibitors of TIMP-4 can be used to treat disorders of corneal and diabetic ulcers and ulcers/lesions caused by microorganisms. Antibodies to TIMP-4 can be used to diagnose such ulcers or lesions. Sequence 675 BP; 154 A; 186 C; 181 G; 154 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-NOV-1997 (first entry)
Tissue inhibitor of metalloproteinase, TIMP-4, cDNA.
Tissue inhibitor of metalloproteinase; TIMP-4; Incyte Clone No. 589345;
metalloprotease; tumour metastasis; angiogenesis; growth; osteoarthriticosteoporosis; pulmonary emphysema; periodontal disease; diabetic ulcer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding a tissue inhibitor of metallo:proteinase(s), for production of recombinant protein for treating tumours arthritis, etc., and for contraception Claim 3; Fig 1; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (INCY-) INCYTE PHARM INC. Hawkins PR, Murry LE; WPI; 97-350238/32.
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T80986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  osteoporosis; pulmonary emphysema; perheumatoid arthritis; contraception;
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8-JAN-1996; US-588163.
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IS5643752-A.
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-tcta-c-acg-gccccctc-ctcggcagtgtgtggggtctcgctggacgttggaggaaa
                                                                                 ccagtatgagatcaagcagataaagatgttcaaagggcctgagaaggatataga
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                                                                                                                                                                                                                                                                                                                                                                                                                      ch 10.0%;
1 Similarity 61.7%;
390; Conservative
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Pred. No. 1.15e-43;
0; Mismatches 233
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                                      22-JUN-1990; U03586.
23-JUN-1989; US-370673.
(GETH ) GENENTECH INC.
Chang M. Goeddel D. Lowe
WPI; 91-036711/05.
N-PSDB; Q10324.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q10572;
                                                                                                                         22-JUN-1990;
23-JUN-1989;
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Modified -site 35..37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= cytoplasmic domain /note= "GC and protien kinase Modified -site 24..26
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                                                                                                                                                                                                                                                                                                               Modified -site
                                                                                                                                                                                                                                                                                                                                                 /label= N-glycos_site
Modified -site 244..246
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                                                                                                                                                                                                                                                                /label= N-glycos_site
wodified -site 349..351
                                                                                                                                                                                                                                                                                                                                                                                          /label= n-glycos_site
Modified -site 195..197
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Modified -site 161..163
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                                                                                                                                                                                                                                                                                                         /label= N-glycos_site
Modified -site 277..279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
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                                                                                                                                                                                                                          N-glycos_site
d -site 600..602
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    protein receptor B
re, heart failure,
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    for diagnosis
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The sequence was derived from the DNA encoding natriuretic peptide receptor B. NPRB, having guanyl cyclase (GC) activity and protein kinase activity. The DNA can be inserted into expression vectors for the prodm. of the protein, opt. after being mutated to produce NPRB analogues. The protein has a mol wt. of 115 kD (calculated Mrainstruretic peptide disorders, and also to isolate peptides using affinity chromatography. Antibodies with affinity for NPRB can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            also be prepd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75 csnynannsavdnknyhdndnnngngcvynaasvarnashwrnnnntagavasgnsaknd 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 ggvrnngarnntnavvnnnhnnsyawawnrvgnavanavnangrannvdnrnvssnnnga 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
mes 77; Conser
                                                                                                                                                                                               nnddnnanyakknntannnnsgnnnnttgmnaadvysngnnnnnnanrsgnnynngndns 732
                                                                                                                                                                                                                                                                                    nnndwmnrysnnndnvkgmannhnsnnsshgsnkssncvvdsrnvnkntdygnasnrsta 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tattccttctttcctccaacgtccagcgagaccccacactgccgaggagggggccgtg
                                                                                                                                                                                                                                                                                                                                                                                               accgctttggccctgatcactacatctgcattgcaaaacg-cctg-ttgcgggtgcaccg 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               yhgvtgnvvmdknndrntdnvnwamgdndsgdnnnaahysganknnwwtgrnnnwvkgan 432
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                                                                                                                                       nknnvnkvrngnrnynrnsndrtnnnnnnvnnmnrcwandnanrndngnnkgnnrrnnkn 792
                                                                                                                                                                         ccagccgcagggtgcgggccgcgcccatggcgggccgggggggctggggggcgggggg 224
                                                                                                                                                                                                                                                                                                                                                                                                                   nsdnnncandnddnscdktnnstnanvangtgntnnmngvssnnnnrknmnnknnasmnw 492
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                            99tsnndnnnnrmnnyannnnknvnnrtnaynnnkrkanannynnnnhsvannnkrgntv 852
                                                                                                     tgagccggggccga-ggcgggcccctcccgcgcgcgctcaccctcctcacctgccccgctc
                                                                                                                                                                                                                                                                                                                       999a9cagctgcaggcgtcggccgggcgaagcagcgtcgccagcagcaggaggccgagcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nnnrarndngvnngnsnmnnnagcnydgnnnyanvnnntnnnggtrndgnrnvnkmngrr 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            yndvngnsnragntratgrnwndnrtrnnananrnann-tvnvntyrnnnnnnynnnnnr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nnsvnhnvyarnnggnnnathnnrangrnvyncgnnnmnhnnnnnanrnnntngd-yvnn 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tccggggaggatgtagcacgggatcatggggcagcgcgtgatcttgcactcgcagccc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative 228; Mismatches 544; Indels
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9.0%;
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Pred. No. 3.92e-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1047
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                                                                                                                                       Matches
                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                 Natriuretic protein receptor B - for diagnosis and treatment of kidney failure, heart failure, hyperaldosteronism, glaucoma etc. Claim 3; Fig 1; 49pp; English.

The sequence was derived from the DNA encoding natriuretic peptide receptor B, NRRB, having guanyl cyclase (GC) activity and protein kinase activity. The DNA can be inserted into expression vectors for the prodn. of the protein, opt. after being mutated to produce NPRB analogues. The protein has a mol wt. of 115 kD (calculated Mr-114,952). The protein (or variants) can be used in treatment of natriuretic peptide disorders, and also to isolate peptides using affinity chromatography. Antibodies with affinity for NPRB can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q10572;
09-APR-1991 (first entry)
                                                                                                                                                                                                                                       also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC.
Chang M, Goeddel D, Lowe
WPI; 91-036711/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-JUN-1990;
23-JUN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Natriuretic Peptide Receptor B. NPRB; ANP; BNP; CNP; kidney failure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q10572 standard; DNA; 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; Q10324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9100292-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified -site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= N-glycos_site
Modified -site 277...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= N-glycos_site
Modified -site 244..246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= N-glycos_site
Modified -site 35..3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= *GC and protien kinase Modified -site 24..26
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493 rnrwnnnngnsnryhkgagsrntnsnrgssygsnmtahgkynnnantghnkgnvvankh 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified -site
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Modified -site 161..163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide 1..22
/label= signal sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                               434 sdnnncandnddnscdktnnstnanvangtgntnnmngvssnnnnrknmnnknnas-mnw 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "binds natriuretic peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nyperaldosteronism; glaucoma; guanyl cyclase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'label= transmembrane domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'label= extracellular domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'label= mature NPBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     label- cytoplasmic domain
                                                            66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45 aattcgccgggcgggg 30
                                                        cgcgcccccgagacaaagaggagaaagtttgcgcggccgagcggggcaggtgaggagg 125
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d -site 195..197
                                                                                                                                                                                                                 prepd.
e 1047 BP;
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d -site 600..6
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d -site 349...
                                                                                                                                                          Similarity
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US-370673.
                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..602
                                                                                                                                                        6.7%;
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                                                                                                                                                                                                                   87 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ö
                                                                                                                                   Score 69; DB 2; Length 1047;
Pred. No. 7,50e-24;
181; Mismatches 361; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 activity"
                                                                                                                                                                                                                   15 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, B and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               heart failure;
                                                                                                                                                                                                                 83 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2
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         Query Match
Best Local S
Matches 17
                                                                                                         cell disorders, etc., etc., call disorders, etc., etc., call disorders, etc., example 4; Page 69-70; 112pp; English.

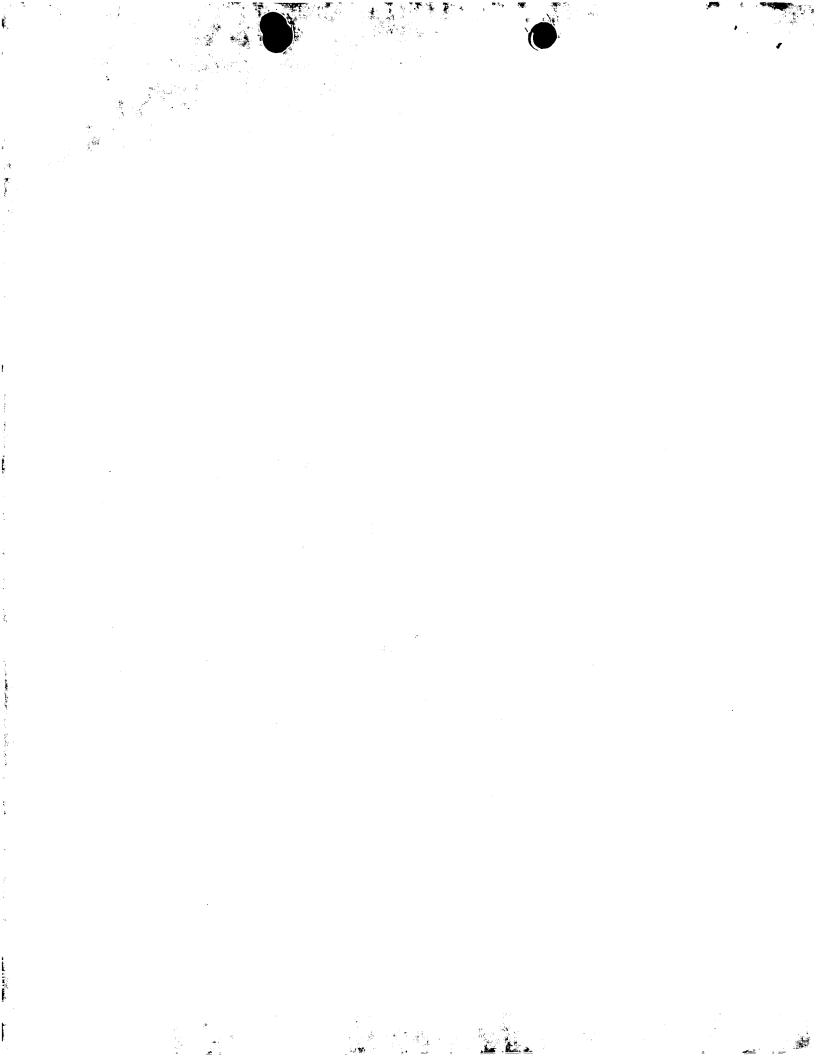
cDNA clone Timp3HCM-3 (T02351) codes for a natural variant (R84217) of tissue inhibitor metalloproteinase 3 (TIMP-3), lacking a portion of the N-terminus of the mature protein in comparison with the clone Timp3clone 7 product (R84215) Timp3HCM-3 was isolated from a human colonic mucosa cDNA library using primers based on TIMP sequences. The cDNA is pref. expressed in Escherich: coll for use in recombinant TIMP-3 product (R84215) Timp3HCM-3 was also be useful for gene therapy e.g. of emphysema.

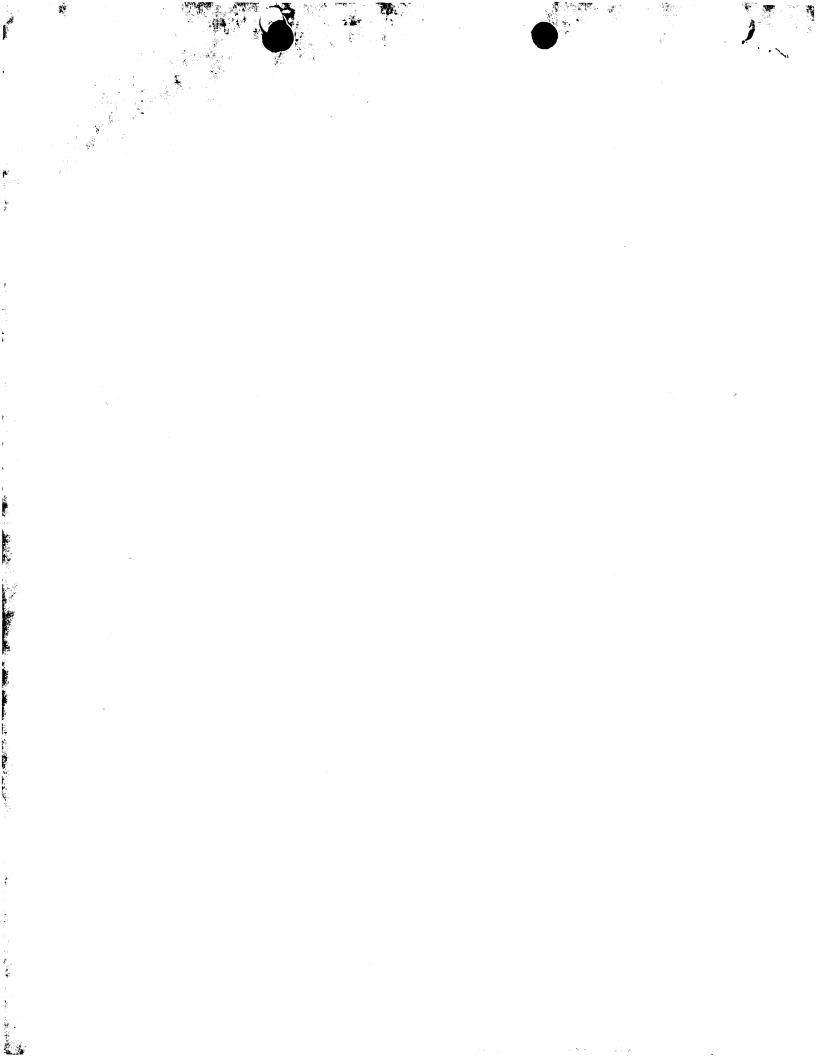
Sequence 820 BP; 204 A; 225 C; 188 G; 203 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inflammation; emphysema; embryo implant modulation; adustrophic epidermolysis bullosa; peridontal disease; scleroderma; vulnerary; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                          New tissue inhibitor metallo:proteinase cancer, inflammation, emphysema, embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; R842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-OCT-1993; US-134231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-OCT-1994; U11241.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9509918-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIMP-3; tissue inhibitor metalloproteinase type three; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-FEB-1996 (first entry)
TIMP-3 clone Timp3HCM-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Koski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AMGE-)
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         h 6.3%;
Similarity 61.8%;
170; Conservative
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            Mismatches 105;
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1.38e-21
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Best Local
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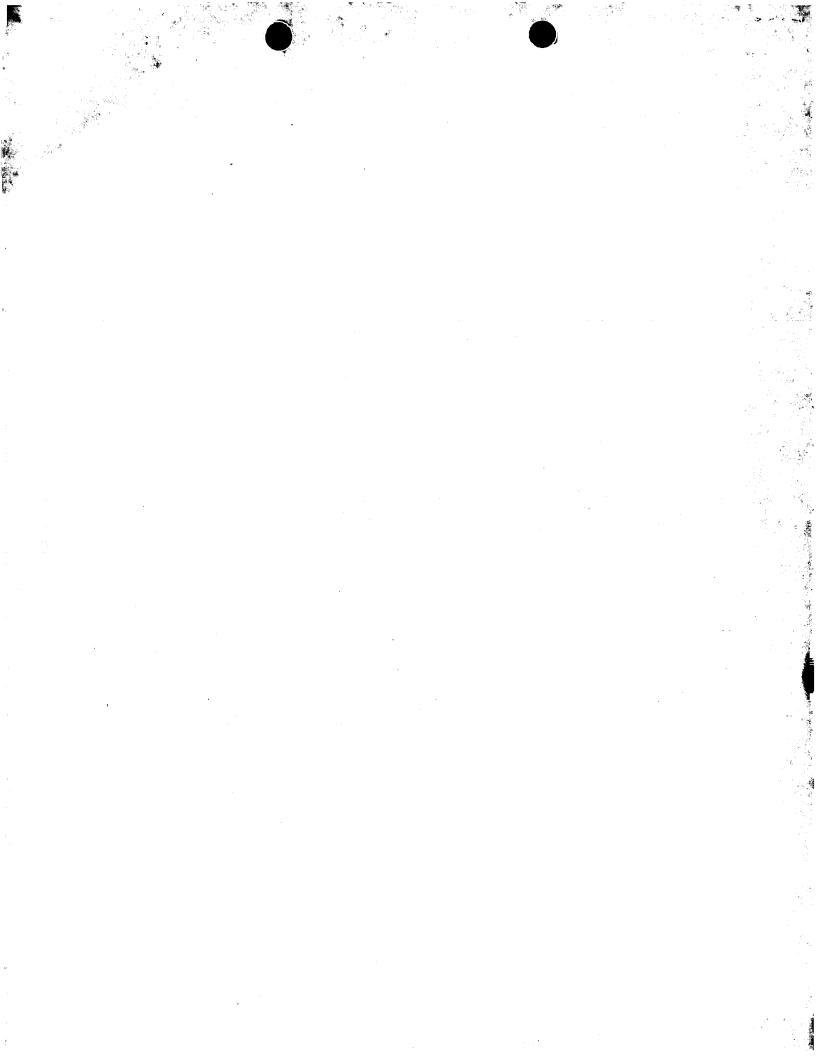
Example 4; Page 67-68; 112pp; English.

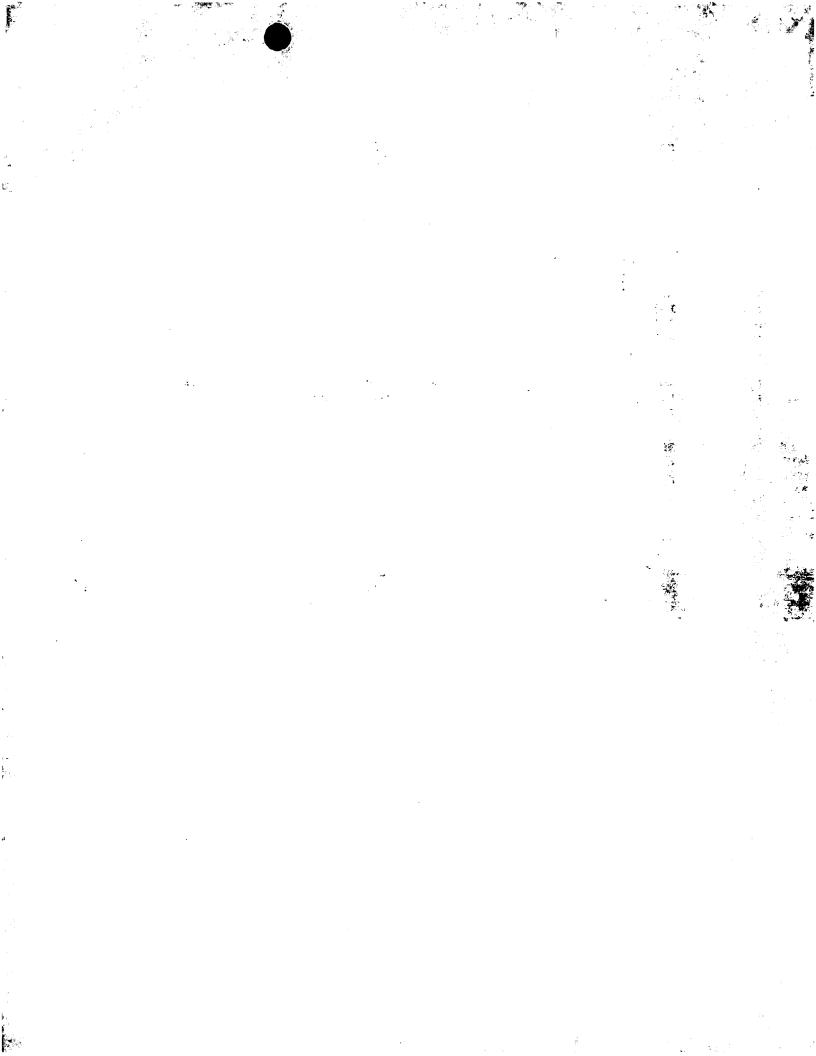
CDNA clone Timp3clone2 (T02360) codes for a natural variant (R84216) of tissue inhibitor metalloproteinase 3 (TIMP-3), lacking part of the signal peptide of the Timp3clone 7 product (R84215). The cDNA clone was isolated from a human 20 and 24 wk foetal kidney cDNA library using primers based on TIMP sequences. The cDNA is pref. expressed in Escherichia coli for use in recombinant TIMP-3 prodn. Genes coding for TIMP may also be useful for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                     e.g. of emphysema.
Sequence 963 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIMP-3 DNA clone Timp3-clone2.
TIMP-3; tissue inhibitor metalloproteinase type three; inflammation; emphysema; embryo implant modulation; art dystrophic epidermolysis bullosa; peridontal disease; u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New tissue inhibitor metallo:proteinase type three - for trocancer, inflammation, emphysema, embryo implant modulation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; R84216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 95-155259/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Koski RA,
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WO9509918-A1.
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llarity 61.8%;
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Pred. No. 1.38e-21;
0; Mismatches 105
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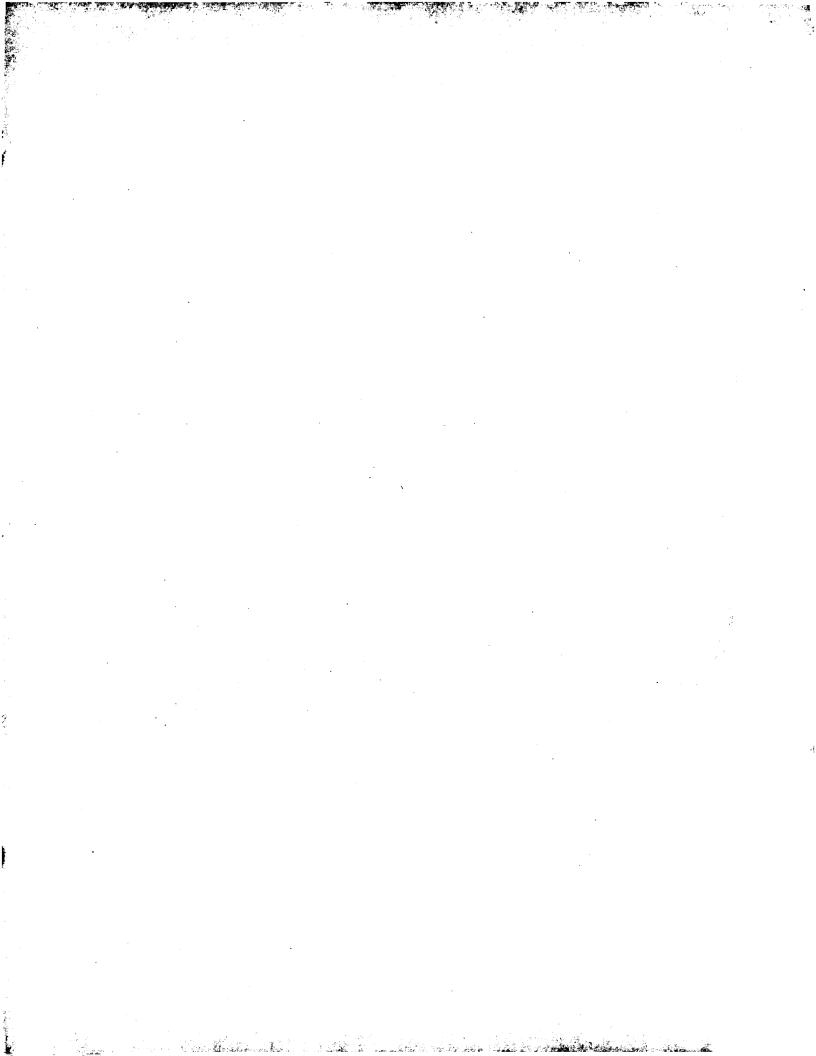


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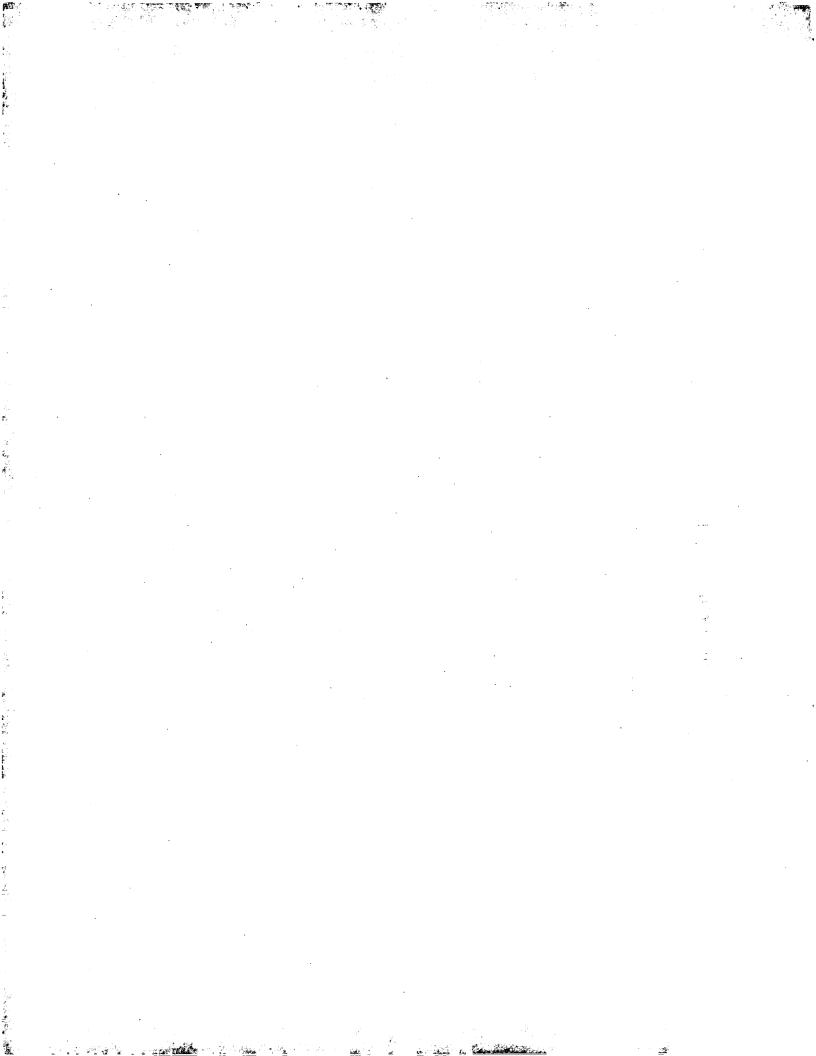
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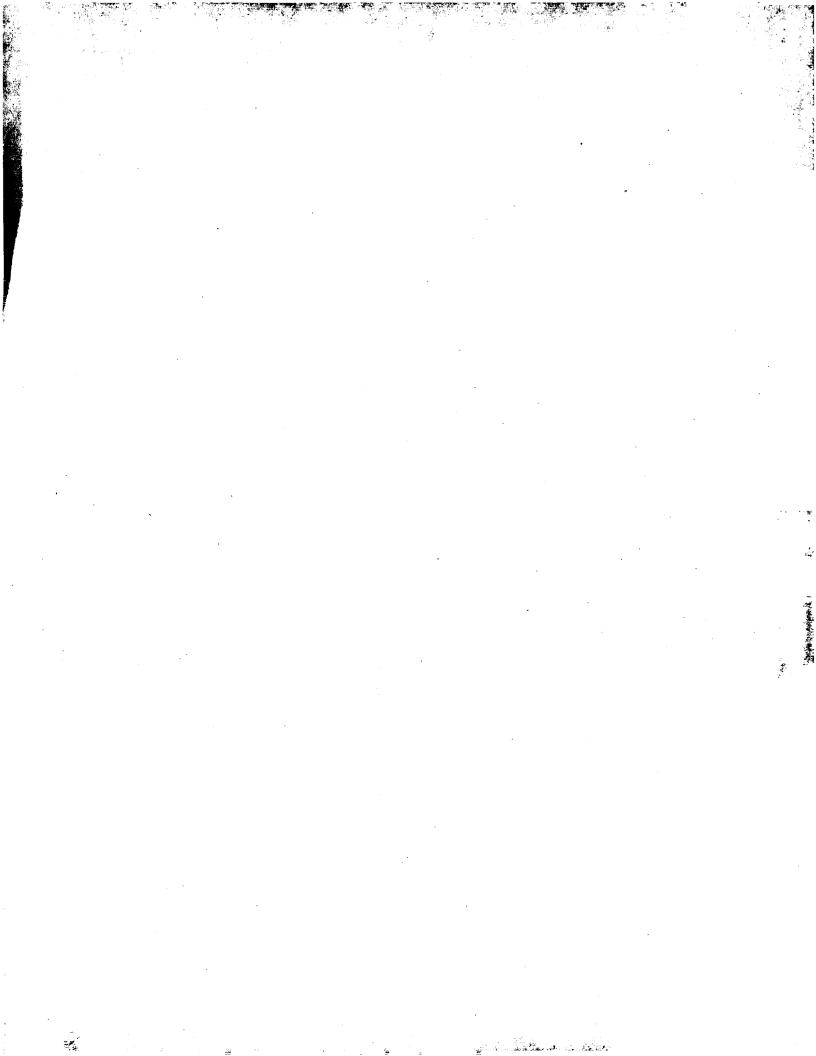


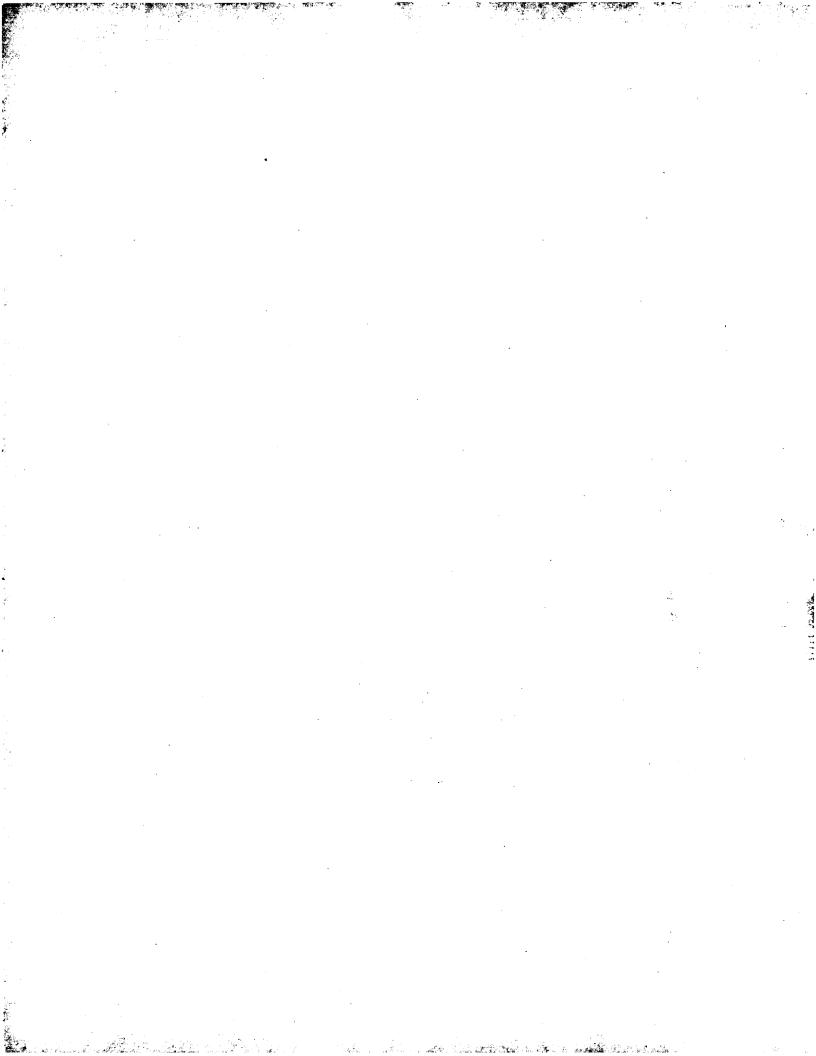
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ΑU
     Division of Dermatology, Washington University School of Medicine,
CS
     St. Louis, Missouri 63110.
     AR 39427 (NIAMS)
NC
     AR 12129 (NIAMS)
     AR 07284 (NIAMS)
     JOURNAL OF BIOLOGICAL CHEMISTRY, (1989 Oct 15) 264 (29)
SO
     17213-21.
     Journal code: HIV. ISSN: 0021-9258.
     United States
CY
     Journal; Article; (JOURNAL ARTICLE)
DT
LA
     English
FS
     Priority Journals; Cancer Journals
os
     GENBANK-J05070
     199001
EM
     ANSWER 3 OF 82 MEDLINE
                                                         DUPLICATE 3
L5
ΑN
     90046765
                  MEDLINE
     90046765
DN
     Human 72-kilodalton type IV collagenase forms a complex with a
ΤI
     tissue inhibitor of metalloproteases designated
     TIMP-2.
     Goldberg G I; Marmer B L; Grant G A; Eisen A Z; Wilhelm S; He C S
     Division of Dermatology, Washington University School of Medicine,
     Saint Louis, MO 63110.
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     OF AMERICA, (1989 Nov) 86 (21) 8207-11.
     Journal code: PV3. ISSN: 0027-8424.
CY
     United States
     Journal; Article; (JOURNAL ARTICLE)
DT
     English
LΑ
     Priority Journals; Cancer Journals
FS
     199002
EM
                                                         DUPLICATE 4
     ANSWER 4 OF 82 MEDLINE
L5
                  MEDLINE
AN
     89109210
     89109210
DN
     Independent regulation of collagenase, 72-kDa progelatinase, and
TI
     metalloendoproteinase inhibitor expression in human fibroblasts by
     transforming growth factor-beta.
     Overall C M; Wrana J L; Sodek J
AU
     Medical Research Council Group in Peridontal Physiology, University
CS
     of Toronto, Ontario, Canada.
SO
     JOURNAL OF BIOLOGICAL CHEMISTRY, (1989 Jan 25) 264 (3)
     1860-9.
     Journal code: HIV. ISSN: 0021-9258.
     United States
CY
     Journal; Article; (JOURNAL ARTICLE)
     Cancer Journals; Priority Journals
FS
     198905
ΕM
     ANSWER 5 OF 82 MEDLINE
                                                         DUPLICATE 5
T.5
ΑN
     90037592
                  MEDLINE
DN
     90037592
     Synovial procollagenase activation by human mast cell tryptase
     dependence upon matrix metalloproteinase 3 activation.
     Gruber B L; Marchese M J; Suzuki K; Schwartz L B; Okada Y; Nagase H;
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Division of Allergy, Rheumatology and Clinical Immunology, Veterans

Ramamurthy N S

CS

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Administration, prthport, New York 11768.
     AR-39189 (NIAMS
NC
     AI-20487 (NIAID)
     DE03987
     JOURNAL OF CLINICAL INVESTIGATION, (1989 Nov) 84 (5)
SO
     Journal code: HS7. ISSN: 0021-9738.
CY
     United States
     Journal; Article; (JOURNAL ARTICLE)
DT
     English
LA
     Abridged Index Medicus Journals; Priority Journals; Cancer Journals
FS
     199002
EM
    ANSWER 6 OF 82 MEDLINE
                                                        DUPLICATE 6
L5
                 MEDLINE
AN
     90026246
     90026246
DN
     Dissociation of tissue inhibitor of metalloproteinases (
ΤI
     TIMP) from enzyme complexes yields fully active inhibitor.
     Murphy G; Koklitis P; Carne A F
AU
     Strangeways Research Laboratory, Cambridge, U.K.
CS
     BIOCHEMICAL JOURNAL, (1989 Aug 1) 261 (3) 1031-4.
SO
     Journal code: 9YO. ISSN: 0264-6021.
CY
     ENGLAND: United Kingdom
     Journal; Article; (JOURNAL ARTICLE)
DT
     English
LΑ
     Priority Journals; Cancer Journals
FS
ΕM
     199001
    ANSWER 7 OF 82 BIOSIS COPYRIGHT 1998 BIOSIS
L5
AN 89:416492 BIOSIS
DN BR37:71955
TI EFFECT OF CYTOKINES ON 72KDA METALLOPROTEINASE AND
  TIMP IN GINGIVAL AND PERIODONTAL LIGAMENT FIBROBLASTS.
AU RICHARDS D; HIBBS M S; RUTHERFORD R B
   UNIV. CONN., FARMINGTON, U.S.A.
SO 67TH GENERAL SESSION OF THE INTERNATIONAL ASSOCIATION FOR DENTAL
    RESEARCH (IADR), 6TH MEETING OF THE IADR IRISH DIVISION, 72ND ANNUAL
    MEETING OF THE SCANDINAVIAN ASSOCIATION FOR DENTAL RESEARCH AND THE
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    DUBLIN, IRELAND, JUNE 28-JULY 1, 1989. J DENT RES 68 (SPEC. ISSUE
    JUNE). 1989. 1019. CODEN: JDREAF ISSN: 0022-0345
DT Conference
LA English
                                                        DUPLICATE 7
     ANSWER 8 OF 82 MEDLINE
L5
AN
     89146140
                 MEDLINE
DN
     89146140
     Antisense RNA-induced reduction in murine TIMP levels
TI
     confers oncogenicity on Swiss 3T3 cells.
     Khokha R; Waterhouse P; Yagel S; Lala P K; Overall C M; Norton G;
ΑU
     Denhardt D T
     Department of Biochemistry, University of Western Ontario, London,
CS
     SCIENCE, (1989 Feb 17) 243 (4893) 947-50.
SO
     Journal code: UJ7. ISSN: 0036-8075.
CY
     United States
     Journal; Article; (JOURNAL ARTICLE)
DT
     English
LA
     Priority Journals; Cancer Journals
FS
EM
    198906
    ANSWER 9 OF 82 BIOSIS COPYRIGHT 1998 BIOSIS
L5
AN 89:281751 BIOSIS
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HUMAN RECOMBINANT TISSUE INHIBITOR OF METALLOPROTEINASE

DN BR37:6748

TIMP INHIBITS NATIVE HUMAN STROMELYSIN IN-VITRO AND AU LARK M W; SAPHOS ; WALAKOVITS L A; MOORE V L CS MERCK SHARP AND DOMME RES. LAB., BIOCHEM. MOL. PATHOL., RAHWAY, N.J. 07065, USA. 73RD ANNUAL MEETING OF THE FEDERATION OF AMERICAN SOCIETIES FOR EXPERIMENTAL BIOLOGY, NEW ORLEANS, LOUISIANA, USA, MARCH 19-23, 1989. FASEB (FED AM SOC EXP BIOL) J 3 (3). 1989. A911. CODEN: FAJOEC ISSN: 0892-6638 DT Conference LA English ANSWER 10 OF 82 MEDLINE DUPLICATE 8 MEDLINE AN89306621 DN 89306621 Genes for extracellular-matrix-degrading metalloproteinases ТT and their inhibitor, TIMP, are expressed during early mammalian development. Brenner C A; Adler R R; Rappolee D A; Pedersen R A; Werb Z ΑU Laboratory of Radiobiology and Environmental Health, University of CS California, San Francisco 94143-0750. HD 23539 (NICHD) NC HD 23651 (NICHD) 5 T32 ES07106 (NIEHS) SO GENES AND DEVELOPMENT, (1989 Jun) 3 (6) 848-59. Journal code: FN3. ISSN: 0890-9369. CY United States Journal; Article; (JOURNAL ARTICLE) DTEnglish LΑ FS Priority Journals 198910 EΜ L5 ANSWER 11 OF 82 MEDLINE DUPLICATE 9 90134705 MEDLINE DN 90134705 Human mesangial cells secrete a GBM-degrading neutral proteinase and TIa specific inhibitor. Martin J; Davies M; Thomas G; Lovett D H ΑU Medical Service, San Francisco VAMC-University of California. CS RO1 DK 39776-01 (NIDDK) NC KIDNEY INTERNATIONAL, (1989 Nov) 36 (5) 790-801. SO Journal code: KVB. ISSN: 0085-2538. CY United States Journal; Article; (JOURNAL ARTICLE) DTLΑ English FS Priority Journals EΜ 199005 ANSWER 12 OF 82 MEDLINE DUPLICATE 10 L5 MEDLINE AN 89340892 89340892 DN Human osteoblasts in vitro secrete tissue inhibitor of ΤI metalloproteinases and gelatinase but not interstitial collagenase as major cellular products. Rifas L; Halstead L R; Peck W A; Avioli L V; Welgus H G ΑU Department of Medicine, Jewish Hospital, Washington University Medical Center, St. Louis, Missouri 63110. AR-32087 (NIAMS) NC AM-35805 (NIADDK) AR-19855 (NIAMS) JOURNAL OF CLINICAL INVESTIGATION, (1989 Aug) 84 (2) SO 686-94.

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Journal; Article; (JOURNAL ARTICLE)

United States

CY

English LA Abridged Index icus Journals; Priority Journa Cancer Journals FS 198911 ΕM DUPLICATE 11 ANSWER 13 OF 82 MEDLINE L5 89340891 MEDLINE AN DN 89340891 Evidence for metalloproteinase and ΤI metalloproteinase inhibitor imbalance in human osteoarthritic cartilage. Dean D D; Martel-Pelletier J; Pelletier J P; Howell D S; Woessner J ΑU Department of Biochemistry & Molecular Biology, University of Miami CS School of Medicine, Florida 33101. AR-16940 (NIAMS) NC AR-08662 (NIAMS) JOURNAL OF CLINICAL INVESTIGATION, (1989 Aug) 84 (2) SO 678-85. Journal code: HS7. ISSN: 0021-9738. United States CYJournal; Article; (JOURNAL ARTICLE) DTLA English Abridged Index Medicus Journals; Priority Journals; Cancer Journals FS 198911 EΜ ANSWER 14 OF 82 BIOSIS COPYRIGHT 1998 BIOSIS T.5 AN 89:329695 BIOSIS DN BR37:32467 TRANSCRIPTIONAL CONTROL OF COLLAGENASE AND TIMP PRODUCTION BY THE HUMAN MONOCYTIC CELL LINE U937. SHAPIRO S D; PARKS W C; LEY T J; KAHN A J; PARTRIDGE N; CAMPBELL E J; ΑU WELGUS H G JEWISH HOSP. AT WASHINGTON UNIV. MED. CENT., ST. LOUIS, MO., USA. CS SO JOINT MEETING OF THE SOCIETY FOR INVESTIGATIVE DERMATOLOGY, EUROPEAN SOCIETY FOR DERMATOLOGIC RESEARCH, AND JAPANESE SOCIETY FOR INVESTIGATIVE DERMATOLOGY, WASHINGTON, D.C., USA, APRIL 26-30, 1989. CLIN RES 37 (2). 1989. 672A. CODEN: CLREAS ISSN: 0009-9279 DT Conference LA English DUPLICATE 12 L5 ANSWER 15 OF 82 MEDLINE MEDLINE 90126366 ΑN 90126366 Developmental expression of tissue inhibitor of metalloproteinase (TIMP) RNA. Nomura S; Hogan B L; Wills A J; Heath J K; Edwards D R ΑU Department of Cell Biology, Vanderbilt University Medical School, CS Nashville, Tennessee 37232. DEVELOPMENT, (1989 Mar) 105 (3) 575-83. SO Journal code: ECW. ISSN: 0950-1991. ENGLAND: United Kingdom CYJournal; Article; (JOURNAL ARTICLE) DTLA English Priority Journals FS ΕM 199005 **DUPLICATE 13** ANSWER 16 OF 82 MEDLINE L5MEDLINE 89206748 ΑN 89206748 DN Characterization of gelatinase from pig polymorphonuclear TIleucocytes. A metalloproteinase resembling tumour type IV collagenase. Murphy G; Ward R; Hembry R M; Reynolds J J; Kuhn K; Tryggvason K

Cell Physiology Department, Strangeways Research Laboratory,

ΑU

CS

Cambridge, U.K.

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BIOCHEMICAL JOUR L, (1989 Mar 1) 258 (2) 463-72 Journal code: 9 ISSN: 0264-6021.
so
     ENGLAND: United Kingdom
CY
     Journal; Article; (JOURNAL ARTICLE)
DT
LΑ
     English
FS
     Priority Journals; Cancer Journals
EΜ
     198907
                                                          DUPLICATE 14
     ANSWER 17 OF 82 MEDLINE
L5
     90093743
ΑN
                  MEDLINE
DN
     90093743
     Matrix metalloproteinases and tissue inhibitor of
TΙ
     metalloproteinases: a review of their role in tumorigenesis
     and tissue invasion.
     Khokha R; Denhardt D T
ΑU
     Cancer Research Laboratory, University of Western Ontario, London,
CS
     Canada.
     INVASION AND METASTASIS, (1989) 9 (6) 391-405. Ref: 72
SO
     Journal code: GV4. ISSN: 0251-1789.
     Switzerland
CY
     Journal; Article; (JOURNAL ARTICLE)
DT
     General Review; (REVIEW)
     (REVIEW, ACADEMIC)
LΑ
     English
     Priority Journals; Cancer Journals
FS
EM
     199004
                                                          DUPLICATE 15
     ANSWER 18 OF 82 MEDLINE
L5
AN
     90022890
                  MEDLINE
DN
     90022890
     Systemic administration of TIMP in the treatment of
TI
     collagen-induced arthritis in mice.
     Carmichael D F; Stricklin G P; Stuart J M
ΑU
CS
     Synergen Inc., Boulder, CO 80301.
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     AGENTS AND ACTIONS, (1989 Jun) 27 (3-4) 378-9.
     Journal code: 2XZ. ISSN: 0065-4299.
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     Switzerland
     Journal; Article; (JOURNAL ARTICLE)
DT
LΑ
     English
FS
     Priority Journals
     199001
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     ANSWER 19 OF 82 MEDLINE
                                                          DUPLICATE 16
L5
AN
     89275215
                 MEDLINE
DN
     89275215
     The role of plasminogen in cell-mediated collagen degradation.
TT
     Gavrilovic J; Murphy G
ΑIJ
     Cell Physiology Department, Strangeways Research Laboratory,
CS
     Cambridge, U.K.
     CELL BIOLOGY INTERNATIONAL REPORTS, (1989 Apr) 13 (4)
SO
     367-75.
     Journal code: CRC. ISSN: 0309-1651.
     ENGLAND: United Kingdom
CY
     Journal; Article; (JOURNAL ARTICLE)
DT
LA
     English
     Priority Journals
FS
EΜ
     198909
                                                          DUPLICATE 17
L5
     ANSWER 20 OF 82 MEDLINE
     90136309
                  MEDLINE
ΑN
DN
     90136309
     Association of collagenase and tissue inhibitor of
ΤI
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enlargement in the growth plate. Dean D D; Muniz O E; Howell D S

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Arthritis Research Laboratory, U.S. Veterans Administration Medical
     Center, Miami,
     AR-08662 (NIAMS)
NC
     MATRIX, (1989 Nov) 9 (5) 366-75.
SO
    Journal code: M54. ISSN: 0934-8832.
     GERMANY, WEST: Germany, Federal Republic of
CY
     Journal; Article; (JOURNAL ARTICLE)
DT
LΑ
     English
     Priority Journals
FS
EΜ
     199005
    ANSWER 21 OF 82 MEDLINE
                                                         DUPLICATE 18
L5
     89230068
                 MEDLINE
NΑ
DN
     89230068
     The effect of lipopolysaccharide from bacteroides gingivalis and
ΤI
     muramyl dipeptide on osteoblast collagenase release.
     Sismey-Durrant H J; Atkinson S J; Hopps R M; Heath J K
ΑU
     Department of Oral Pathology, London Hospital Medical College,
CS
     England.
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     CALCIFIED TISSUE INTERNATIONAL, (1989 May) 44 (5) 361-3.
     Journal code: CGH. ISSN: 0171-967X.
     GERMANY, WEST: Germany, Federal Republic of
CY
     Journal; Article; (JOURNAL ARTICLE)
DT
LΑ
     English
FS
     Priority Journals
EM
     198908
                                                         DUPLICATE 19
L5
     ANSWER 22 OF 82 MEDLINE
ΑN
     89375511
                  MEDLINE
     89375511
DN
     The enzymatic evaluation of procollagenase and collagenase
TI
     inhibitors in crude biological media.
     Lefebvre V; Vaes G
ΑU
     Laboratoire de Chimie Physiologique, Universite de Louvain,
CS
     Brussels, Belgium.
     BIOCHIMICA ET BIOPHYSICA ACTA, (1989 Sep 15) 992 (3)
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     Journal code: AOW. ISSN: 0006-3002.
CY
     Netherlands
     Journal; Article; (JOURNAL ARTICLE)
DT
T.A
     English
FS
     Priority Journals; Cancer Journals
EM
     198912
    ANSWER 23 OF 82 BIOSIS COPYRIGHT 1998 BIOSIS
L5
    89:151284 BIOSIS
AN
DN
   BR36:73325
    FORMATION OF NEUTRAL PROTEINASE NP COLLAGEN IV CIV AND TISSUE
    INHIBITOR OF METALLOPROTEINASES TIMP BY RESTING
    AND PROLIFERATING MESANGIAL CELLS MCS IN CULTURE.
   GROUND J; LOVETT D H; COFFEE M; KASHGARIAN M; STERZEL R B
   VAMC-YALE UNIV. SCH. MED., NEW HAVEN, CONN.
   MEETING OF THE AMERICAN SOCIETY OF NEPHROLOGY, SAN ANTONIO, TEXAS,
    USA, DECEMBER 11-14, 1988. KIDNEY INT 35 (1). 1989. 348. CODEN:
    KDYIA5 ISSN: 0085-2538
LA English
    ANSWER 24 OF 82 MEDLINE
ΑN
     90125644
                  MEDLINE
DN
     90125644
     Transforming growth factor-beta regulation of collagenase, 72
TΙ
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TI Transforming growth factor-beta regulation of collagenase, 72 kDa-progelatinase, TIMP and PAI-1 expression in rat bone cell populations and human fibroblasts.

AU Overall C M; Wrana J L; Sodek J

CS Medical Research Council Group in Periodontal Physiology, University

of Toronto, Ontário, Canada. CONNECTIVE TISS RESEARCH, (1989) 20 (1-4) 289-Journal code: Don. ISSN: 0300-8207. so CY ENGLAND: United Kingdom Journal; Article; (JOURNAL ARTICLE) DT LΑ English FS Priority Journals EM 199005 ANSWER 25 OF 82 MEDLINE L5 AN 90014493 MEDLINE DN 90014493 Metalloproteinases are not involved in the phagocytosis of TI collagen fibrils by fibroblasts. Everts V; Hembry R M; Reynolds J J; Beertsen W ΑU CS Laboratory of Histology and Cell Biology, Faculty of Medicine, University of Amsterdam, The Netherlands. MATRIX, (1989 Aug) 9 (4) 266-76.

Journal code: M54. ISSN: 0934-8832. SO GERMANY, WEST: Germany, Federal Republic of CY Journal; Article; (JOURNAL ARTICLE) DTEnglish LA FS Priority Journals EΜ 199001 ANSWER 26 OF 82 BIOSIS COPYRIGHT 1998 BIOSIS T.5 AN 89:244735 BIOSIS DN BA87:125800 REGIONAL LOCALIZATION OF THE TIMP GENE ON THE HUMAN X CHROMOSOME EXTENSION OF A CONSERVED SYNTENY AND LINKAGE GROUP ON PROXIMAL XP. AU WILLIARD H F; DURFY S J; MAHTANI M M; DORKINS H; DAVIES K E; WILLIAMS BRG CS DEP. MED. GENETICS, UNIV. TORONTO, MED. SCI. BUILDING 4282, TORONTO, ONTARIO M5S 1A8, CANADA. HUM GENET 81 (3). 1989. 235-238. CODEN: HUGEDQ ISSN: 0340-6717 LA English L5 ANSWER 27 OF 82 MEDLINE 89154429 MEDLINE ΑN DN 89154429 Regional localization of the TIMP gene on the human X chromosome. Extension of a conserved synteny and linkage group on proximal Xp. Willard H F; Durfy S J; Mahtani M M; Dorkins H; Davies K E; Williams ΑU Department of Medical Genetics, University of Toronto, Ontario, Canada. HUMAN GENETICS, (1989 Feb) 81 (3) 234-8. Journal code: GED. ISSN: 0340-6717. CY GERMANY, WEST: Germany, Federal Republic of DT Journal; Article; (JOURNAL ARTICLE) LA English FS Priority Journals; Cancer Journals EM 198906 DUPLICATE 20 L5 ANSWER 28 OF 82 MEDLINE AN89141242 MEDLINE 89141242 DN Neutral metalloprotease from tendons. TI Piening C; Riederer-Henderson M A ΑU Department of Orthopaedics, University of Washington, Seattle CS

JOURNAL OF ORTHOPAEDIC RESEARCH, (1989) 7 (2) 228-34.

Journal code: JIQ. ISSN: 0736-0266.

98195..

SO

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CY
     United States
                       (JOURNAL ARTICLE)
     Journal; Articl
DT
LА
     English
     Priority Journals
FS
EΜ
     198906
     ANSWER 29 OF 82 MEDLINE
L5
     90007512 MEDLINE
ΑN
     90007512
DN
     Linkage studies of the Wiskott-Aldrich syndrome: polymorphisms at
ΤI
     TIMP and the X chromosome centromere are informative markers
     for genetic prediction.
     Greer W L; Mahtani M M; Kwong P C; Rubin L A; Peacocke M; Willard H
ΑU
     F; Siminovitch K A
     Department of Medicine, Toronto Western Hospital, Ontario, Canada.
CS
     HUMAN GENETICS, (1989 Oct) 83 (3) 227-30.
SO
     Journal code: GED. ISSN: 0340-6717.
     GERMANY, WEST: Germany, Federal Republic of
CY
     Journal; Article; (JOURNAL ARTICLE)
DT
LΑ
     English
     Priority Journals; Cancer Journals
FS
     199001
EM
     ANSWER 30 OF 82 MEDLINE
                                                         DUPLICATE 21
L5
ΑN
     89382034
                 MEDLINE
     89382034
DN
     Gingival fibroblasts degrade type I collagen films when stimulated
ΤI
     with tumor necrosis factor and interleukin 1: evidence that
     breakdown is mediated by metalloproteinases.
     Meikle M C; Atkinson S J; Ward R V; Murphy G; Reynolds J J
ΑU
     JOURNAL OF PERIODONTAL RESEARCH, (1989 May) 24 (3) 207-13.
     Journal code: JMQ. ISSN: 0022-3484.
CY
     Denmark
DT
     Journal; Article; (JOURNAL ARTICLE)
     English
LA
FS
     Dental Journals
     198912
EM
    ANSWER 31 OF 82 MEDLINE
                                                        DUPLICATE 22
L5
     90104231
                 MEDLINE
ΑN
DN
     90104231
     Fragments of human fibroblast collagenase. Purification and
TI
     characterization.
ΑU
     Clark I M; Cawston T E
     Rheumatology Research Unit, Addenbrooke's Hospital, Cambridge, U.K.
CS
SO
     BIOCHEMICAL JOURNAL, (1989 Oct 1) 263 (1) 201-6.
     Journal code: 9YO. ISSN: 0264-6021.
CY
     ENGLAND: United Kingdom
     Journal; Article; (JOURNAL ARTICLE)
DT
LΑ
     English
FS
     Priority Journals; Cancer Journals
EΜ
     199004
                                                        DUPLICATE 23
L5
     ANSWER 32 OF 82 MEDLINE
     89263367
                 MEDLINE
ΑN
     89263367
DN
     [Natural inhibitor of metalloproteinases: structural and
     functional study].
     Inhibiteur naturel des metalloproteinases: etude
     structurale et fonctionnelle.
     Faucher D; Leli`evre Y; Boiziau J; Cornet P; Cartwright T
     Rhone-Poulenc Sante (CRMA), Site de Recherche de Monts, France.
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Journal code: OSG. ISSN: 0369-8114.

CY

France

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Journal; Article (JOURNAL ARTICLE)
     French
LA
     Priority Journal
FS
     198909
EΜ
    ANSWER 33 OF 82 BIOSIS COPYRIGHT 1998 BIOSIS
L5
    89:236476 BIOSIS
AN
DN BR36:114960
TI EFFECTS OF RECOMBINANT TIMP ON BONE RESORPTION BY ISOLATED
    OSTEOCLASTS.
AU SHIMIZU H; SAKAMOTO M; SAKAMOTO S
CS HARV. SCH. DENTAL MED., BOSTON, MASS., USA.
SO 18TH ANNUAL SESSION OF THE AMERICAN ASSOCIATION FOR DENTAL RESEARCH,
    SAN FRANCISCO, CALIFORNIA, USA, MARCH 15-19, 1989. J DENT RES 68 (SPEC. ISSUE). 1989. 193. CODEN: JDREAF ISSN: 0022-0345
    Conference
LA English
L5
     ANSWER 34 OF 82 MEDLINE
                                                           DUPLICATE 24
ΑN
     90023570
                  MEDLINE
     90023570
DN
     Increased immunostaining of collagenase and TIMP in
TI
     eruptive xanthoma.
ΑU
     Childers J W; Stricklin G P
     Section of Dermatology, Medical Service VA Medical Center,
     Nashville, TN 37212.
SO
     AMERICAN JOURNAL OF THE MEDICAL SCIENCES, (1989 Sep) 298
     (3) 172-6.
     Journal code: 3L2. ISSN: 0002-9629.
CY
     United States
DT
     Journal; Article; (JOURNAL ARTICLE)
LΑ
FS
     Abridged Index Medicus Journals; Priority Journals
ĒΜ
     199001
L5
     ANSWER 35 OF 82 MEDLINE
                                                           DUPLICATE 25
     90005712
                   MEDLINE
ΑN
     90005712
DN
     Replicative senescence of human skin fibroblasts correlates with a
     loss of regulation and overexpression of collagenase activity.
ΑU
     West M D; Pereira-Smith O M; Smith J R
     Roy M. and Phyllis Gough Huffington Center on Aging, Baylor College
     of Medicine, Houston, Texas 77030.
NC
     AG-04749 (NIA)
     AG-05333 (NIA)
     PO1-AG-07123 (NIA)
SO
     EXPERIMENTAL CELL RESEARCH, (1989 Sep) 184 (1) 138-47.
     Journal code: EPB. ISSN: 0014-4827.
     United States
CY
     Journal; Article; (JOURNAL ARTICLE)
DT
LΑ
     English
FS
     Priority Journals; Cancer Journals
    ANSWER 36 OF 82 BIOSIS COPYRIGHT 1998 BIOSIS
L5
AN 90:38514 BIOSIS
    BR38:17744
TI TIMP-2 COMPLETE PRIMARY STRUCTURE OF A NOVEL MEMBER OF THE
  TIMP FAMILY.
AU STETLER-STEVENSON W G; KRUTZSCH H; LIOTTA L A
    LAB. PATHOL., NATL. CANCER INST., BETHESDA, MD. 20879, USA.
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1989. 136A. CODEN: JCLBA3 ISSN: 0021-9525

DT Conference

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- AN 90:38512 BIOSIS
- DN BR38:17742
- TI TRANSCRIPTIONAL CONTROL OF COLLAGENASE AND TIMP PRODUCTION BY THE HUMAN MONOCYTIC CELL LINE U937.
- AU SHAPIRO S D; PARKS W C; LEY T J; KAHN A J; PARTRIDGE N; CAMPBELL E J; WELGUS H G
- CS JEWISH HOSP. AT WASHINGTON UNIV. MED. CENT., ST. LOUIS, MO.
- SO TWENTY-NINTH ANNUAL MEETING OF THE AMERICAN SOCIETY FOR CELL BIOLOGY, HOUSTON, TEXAS, USA, NOVEMBER 5-9, 1989. J CELL BIOL 109 (4 PART 2). 1989. 135A. CODEN: JCLBA3 ISSN: 0021-9525
- DT Conference
- LA English
- L5 ANSWER 38 OF 82 BIOSIS COPYRIGHT 1998 BIOSIS
- AN 89:401034 BIOSIS
- DN BA88:70459
- TI A HIGH MOLECULAR WEIGHT COLLAGENASE INHIBITOR MADE BY RABBIT CHONDROCYTES IN CELL CULTURE.
- AU MORRIS G M
- CS DEP. PHARMACOL., STATE UNIV. NEW YORK STONY BROOK, STONY BROOK, N.Y. 11794-8651, USA.
- SO MATRIX 9 (2). 1989. 127-134. CODEN: MTRXEH
- LA English
- L5 ANSWER 39 OF 82 MEDLINE

DUPLICATE 26

- AN 90057454 MEDLINE
- DN 90057454
- TI Type I collagen degradation by mouse calvarial osteoblasts stimulated with 1,25-dihydroxyvitamin D-3: evidence for a plasminogen-plasmin-metalloproteinase activation cascade.
- AU Thomson B M; Atkinson S J; McGarrity A M; Hembry R M; Reynolds J J; Meikle M C
- CS Cell Physiology Department, Strangeways Research Laboratory, Worts Causeway, Cambridge, U.K.
- SO BIOCHIMICA ET BIOPHYSICA ACTA, (1989 Nov 20) 1014 (2) 125-32.
 - Journal code: AOW. ISSN: 0006-3002.
- CY Netherlands
- DT Journal; Article; (JOURNAL ARTICLE)
- LA English
- FS Priority Journals; Cancer Journals
- EM 199003
- L5 ANSWER 40 OF 82 MEDLINE

DUPLICATE 27

- AN 89292024 MEDLINE
- DN 89292024
- TI Down-regulation of proteolytic activity in 12-0-tetradecanoyl-phorbol-13-acetate-induced K562 leukemia cell cultures: depletion of active urokinase by excess type 1 plasminogen activator inhibitor.
- AU Alitalo R; Andersson L C; Tapiovaara H; Sistonen L; Vaheri A; Stephens R
- CS Transplantation Laboratory, University of Helsinki, Finland.
- SO JOURNAL OF CELLULAR PHYSIOLOGY, (1989 Jul) 140 (1) 119-30. Journal code: HNB. ISSN: 0021-9541.
- CY United States
- DT Journal; Article; (JOURNAL ARTICLE)
- LA English
- FS Priority Journals; Cancer Journals
- EM 198910
- L5 ANSWER 41 OF 82 BIOSIS COPYRIGHT 1998 BIOSIS
- AN 90:24704 BIOSIS

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DN BA89:11670
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    COLLAGEN FIBRILS BY FIBROBLASTS.
AU EVERTS V; HEMBRY R M; REYNOLDS J J; BEERTSEN W
CS LAB. HISTOL. CELL BIOL., ACAD. MED. CENT., MEIBERGDREEF 15, 1105 AZ
   AMSTERDAM, NETHERLANDS.
   MATRIX 9 (4). 1989. 66-76. CODEN: MTRXEH
SO
LΑ
   English
     ANSWER 42 OF 82 MEDLINE
L5
     90107445
                  MEDLINE
ΑN
     90107445
DN
     Expression of genes for non-collagenous proteins during embryonic
ΤI
     bone formation.
ΑU
     Nomura S; Wills A J; Edwards D R; Heath J K; Hogan B L
     Department of Cell Biology, Vanderbilt University Medical School,
CS
    Nashville, TN 37232.
SO
     CONNECTIVE TISSUE RESEARCH, (1989) 21 (1-4) 31-5;
     discussion 36-9. Ref: 22
     Journal code: DQH. ISSN: 0300-8207.
CY
     ENGLAND: United Kingdom
     Journal; Article; (JOURNAL ARTICLE)
     General Review; (REVIEW)
     (REVIEW, TUTORIAL)
LΑ
     English
FS
     Priority Journals
EM
     199004
L5
     ANSWER 43 OF 82 MEDLINE
                                                         DUPLICATE 28
AN
     88327732
                  MEDLINE
DN
     88327732
TΙ
     Inhibition by human recombinant tissue inhibitor of
     metalloproteinases of human amnion invasion and lung
     colonization by murine B16-F10 melanoma cells.
     Schultz R M; Silberman S; Persky B; Bajkowski A S; Carmichael D F
ΑU
     Department of Biochemistry, Loyola University of Chicago, Stritch
CS
     School of Medicine, Maywood, Illinois 60153.
     CA43305 (NCI)
NC
     CA44659 (NCI)
     CANCER RESEARCH, (1988 Oct 1) 48 (19) 5539-45.
SO
     Journal code: CNF. ISSN: 0008-5472.
CY
     United States
DT
     Journal; Article; (JOURNAL ARTICLE)
LΆ
     English
     Priority Journals; Cancer Journals
FS
EM
     198812
                                                         DUPLICATE 29
L5
     ANSWER 44 OF 82 MEDLINE
     89067507
                  MEDLINE
ΑN
     89067507
DN
     Selective up-regulation of human alveolar macrophage collagenase
TΙ
     production by lipopolysaccharide and comparison to collagenase
     production by fibroblasts.
     Cury J D; Campbell E J; Lazarus C J; Albin R J; Welgus H G
ΑU
     Department of Medicine, Jewish Hospital, St. Louis, MO 63110.
CS
NC
     AM35805 (NIADDK)
     HL29594 (NHLBI)
     5T32-HL07317 (NHLBI)
     JOURNAL OF IMMUNOLOGY, (1988 Dec 15) 141 (12) 4306-12.
SO
     Journal code: IFB. ISSN: 0022-1767.
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United States

English

Journal; Article; (JOURNAL ARTICLE)

CY

DT LA

FS

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198903
EΜ
                                                          OUPLICATE 30
     ANSWER 45 OF 82 MEDLINE
L5
                  MEDLINE
     89096910
ΑN
     89096910
DN
     Presence of transcription regulatory elements within an intron of
\mathtt{TI}
     the virus-inducible murine TIMP gene.
     Coulombe B; Ponton A; Daigneault L; Williams B R; Skup D
ΑU
     Institut du Cancer de Montreal, Quebec, Canada.
CS
     MOLECULAR AND CELLULAR BIOLOGY, (1988 Aug) 8 (8) 3227-34.
SO
     Journal code: NGY. ISSN: 0270-7306.
     United States
CY
     Journal; Article; (JOURNAL ARTICLE)
DT
LΑ
     English
FS
     Priority Journals
os
     GENBANK-M21162
ĒΜ
     198904
                                                         DUPLICATE 31
L5
     ANSWER 46 OF 82 MEDLINE
ΑN
     88222411
                  MEDLINE
DN
     88222411
     K562 cells produce and respond to human erythroid-potentiating
TI
     activity.
     Avalos B R; Kaufman S E; Tomonaga M; Williams R E; Golde D W; Gasson
ΑU
     Department of Medicine, UCLA School of Medicine.
CS
NC
     CA30388 (NCI)
     CA32737 (NCI)
     CA40163 (NCI)
SO
     BLOOD, (1988 Jun) 71 (6) 1720-5.
     Journal code: A8G. ISSN: 0006-4971.
CY
     United States
DT
     Journal; Article; (JOURNAL ARTICLE)
LA
     English
FS
     Abridged Index Medicus Journals; Priority Journals; Cancer Journals
EM
     198809
                                                         DUPLICATE 32
L5
     ANSWER 47 OF 82 MEDLINE
AN
     88087284
                  MEDLINE
DN
     88087284
     In vitro synthesis of the active tissue inhibitor of
ΤI
     metalloproteinases encoded by a complementary DNA from
     virus-infected murine fibroblasts.
     Coulombe B; Skup D
ΑU
     Institut du Cancer de Montreal, Quebec, Canada.
CS
     JOURNAL OF BIOLOGICAL CHEMISTRY, (1988 Jan 25) 263 (3)
SO
     1439-43.
     Journal code: HIV. ISSN: 0021-9258.
     United States
CY
     Journal; Article; (JOURNAL ARTICLE)
DT
LA
     English
     Priority Journals; Cancer Journals
FS
EM
     198804
     ANSWER 48 OF 82 BIOSIS COPYRIGHT 1998 BIOSIS
L5
   89:192412 BIOSIS
AN
DN BR36:92861
TI TISSUE INHIBITOR OF METALLOPROTEINASES TIMP
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BEHRENDTSEN O; ALEXANDER C A; WERB Z

CALIF. 94143-0750.

ΑU

107 (6 PART 3). 1088. 604A. CODEN: JCLBA3 ISSN: 21-9525 Conference

DT Conference

LA English

L5 ANSWER 49 OF 82 BIOSIS COPYRIGHT 1998 BIOSIS

AN 88:345119 BIOSIS

DN BR35:39961

TI MODULATION OF THE COLLAGENASE INHIBITOR **TIMP** MESSENGER RNA LEVELS BY ANTI-SENSE RNA INFLUENCES THE INVASIVENESS OF MOUSE 3T3 CELLS.

AU KHOKHA R; WATERHOUSE P; YAGEL S; LALA P K; NORTON G; DENHARDT D T

- CS CANCER RES. LAB., UNIV. WESTERN ONTARIO, LONDON, ONT. N6A5B7 CANADA.
- SO 79TH ANNUAL MEETING OF THE AMERICAN ASSOCIATION FOR CANCER RESEARCH, NEW ORLEANS, LOUISIANA, USA, MAY 25-28, 1988. PROC AM ASSOC CANCER RES ANNU MEET 29 (0). 1988. 439. CODEN: PAMREA
- DT Conference
- LA English
- L5 ANSWER 50 OF 82 BIOSIS COPYRIGHT 1998 BIOSIS
- AN 89:171617 BIOSIS
- DN BR36:82858
- TI GENES FOR EXTRACELLULAR MATRIX-DEGRADING **METALLOPROTEINASES**AND THEIR INHIBITOR **TIMP** FUNCTION DURING EARLY MAMMALIAN
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- AU BRENNER C A; ADLER R R; RAPPOLEC D A; PEDERSEN R A; BEHRENDTSEN O; WERB Z
- CS LAB. RADIOBIOL. ENVIRON. HEALTH, UNIV. CALIFORNIA, SAN FRANCISCO, CALIF. 94143-0750.
- SO JOINT MEETING OF THE AMERICAN SOCIETY FOR CELL BIOLOGY AND THE AMERICAN SOCIETY FOR BIOCHEMISTRY AND MOLECULAR BIOLOGY, SAN FRANCISCO, CALIFORNIA, USA, JANUARY 29-FEBRUARY 2, 1989. J CELL BIOL 107 (6 PART 3). 1988. 380A. CODEN: JCLBA3 ISSN: 0021-9525
- DT Conference
- LA English
- L5 ANSWER 51 OF 82 MEDLINE
- AN 89110656 MEDLINE
- DN 89110656
- TI Identification of matrix metalloendoproteinase inhibitor (**TIMP**) in human parotid and submandibular saliva: partial purification and characterization.
- AU Drouin L; Overall C M; Sodek J
- SO JOURNAL OF PERIODONTAL RESEARCH, (1988 Nov) 23 (6) 370-7. Journal code: JMQ. ISSN: 0022-3484.
- CY Denmark
- DT Journal; Article; (JOURNAL ARTICLE)
- LA English
- FS Dental Journals
- EM 198905
- L5 ANSWER 52 OF 82 MEDLINE
- AN 88193653 MEDLINE
- DN 88193653
- TI Role of collagenase in colonic anastomoses: a reappraisal.
- AU Chowcat N L; Savage F J; Hembry R M; Boulos P B
- CS Department of Surgery, University College London, UK.
- SO BRITISH JOURNAL OF SURGERY, (1988 Apr) 75 (4) 330-4. Journal code: B34. ISSN: 0007-1323.
- CY ENGLAND: United Kingdom
- DT Journal; Article; (JOURNAL ARTICLE)
- LA English
- FS Abridged Index Medicus Journals; Priority Journals; Cancer Journals
- EM 198808
- L5 ANSWER 53 OF 82 MEDLINE

- AN 88271651 MEN_INE
- DN 88271651
- TI Human recombinant interleukin-1 alpha-mediated stimulation of procollagenase production and suppression of biosynthesis of tissue inhibitor of metalloproteinases in rabbit uterine cervical fibroblasts.
- AU Ito A; Goshowaki H; Sato T; Mori Y; Yamashita K; Hayakawa T; Nagase
- CS Department of Biochemistry, Tokyo College of Pharmacy, Japan.
- NC AR 39189 (NIAMS)
- SO FEBS LETTERS, (1988 Jul 18) 234 (2) 326-30. Journal code: EUH. ISSN: 0014-5793.
- CY Netherlands
- DT Journal; Article; (JOURNAL ARTICLE)
- LA English
- FS Priority Journals; Cancer Journals
- EM 198810
- L5 ANSWER 54 OF 82 MEDLINE

DUPLICATE 33

- AN 88115581 MEDLINE
- DN 88115581
- TI Modulation of fibroblast functions by interleukin 1: increased steady-state accumulation of type I procollagen messenger RNAs and stimulation of other functions but not chemotaxis by human recombinant interleukin 1 alpha and beta.
- AU Postlethwaite A E; Raghow R; Stricklin G P; Poppleton H; Seyer J M; Kang A H
- CS Department of Medicine, University of Tennessee, Memphis 38163.
- NC AM 16506 (NIADDK) AM 26034 (NIADDK)
- SO JOURNAL OF CELL BIOLOGY, (1988 Feb) 106 (2) 311-8.
 - Journal code: HMV. ISSN: 0021-9525.
- CY United States
- DT Journal; Article; (JOURNAL ARTICLE)
- LA English
- FS Priority Journals; Cancer Journals
- EM 198805
- L5 ANSWER 55 OF 82 BIOSIS COPYRIGHT 1998 BIOSIS
- AN 88:370588 BIOSIS
- DN BR35:55201
- TI MODULATION OF THE COLLAGENASE INHIBITOR **TIMP** MESSENGER RNA LEVELS BY ANTI-SENSE RNA INFLUENCES THE INVASIVENESS OF MOUSE 3T3 CELLS.
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- CS CANCER RES. LAB., UNIV. WEST. ONT., LONDON, ONT., CAN.
- SO SYMPOSIUM ON CELLULAR PROTEASES AND CONTROL MECHANISMS HELD AT THE 17TH ANNUAL UCLA (UNIVERSITY OF CALIFORNIA-LOS ANGELES) MEETING ON MOLECULAR AND CELLULAR BIOLOGY, LAKE TAHOE, CALIFORNIA, USA, FEBRUARY 21-26, 1988. J CELL BIOCHEM SUPPL 0 (12 PART B). 1988. 290. CODEN: JCBSD7
- DT Conference
- LA English
- L5 ANSWER 56 OF 82 BIOSIS COPYRIGHT 1998 BIOSIS
- AN 88:238354 BIOSIS
- DN BR34:120874
- TI IDENTIFICATION AND PURIFICATION OF COLLAGENASE INHIBITOR TIMP IN HUMAN PAROTID AND SUBMANDIBULAR SALIVA.
- AU DROUIN L; OVERALL C M; SODEK J
- CS MED. RES. COUNCIL GROUP PERIODONTAL PHYSIOL., UNIV. TORONTO, TORONTO, ONTARIO, CAN.
- SO 66TH GENERAL SESSION OF THE INTERNATIONAL ASSOCIATION FOR DENTAL RESEARCH, 17TH ANNUAL SESSION OF THE AMERICAN ASSOCIATION FOR DENTAL RESEARCH, AND 12TH ANNUAL MEETING OF THE CANADIAN ASSOCIATION FOR

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- DT Conference
- LA English
- L5 ANSWER 57 OF 82 BIOSIS COPYRIGHT 1998 BIOSIS
- AN 88:238145 BIOSIS
- DN BR34:120665
- TI POLYCLONAL ANTIBODIES TO 3 SYNTHETIC PEPTIDES DERIVED FROM THE CONSENSUS SEQUENCE OF TIMP.
- AU BODDEN M K; BIRKEDAL-HANSEN H
- CS UNIV. ALA. SCH. DENT., BIRMINGHAM, ALA.
- SO 66TH GENERAL SESSION OF THE INTERNATIONAL ASSOCIATION FOR DENTAL RESEARCH, 17TH ANNUAL SESSION OF THE AMERICAN ASSOCIATION FOR DENTAL RESEARCH, AND 12TH ANNUAL MEETING OF THE CANADIAN ASSOCIATION FOR DENTAL RESEARCH, MONTREAL, QUEBEC, CANADA, MARCH 9-13, 1988. J DENT RES 67 (SPEC. ISSUE MAR.). 1988. 210. CODEN: JDREAF ISSN: 0022-0345
- DT Conference
- LA English
- L5 ANSWER 58 OF 82 MEDLINE

DUPLICATE 34

- AN 89138439 MEDLINE
- DN 89138439
- TI Multilocus molecular mapping of the mouse X chromosome.
- AU Mullins L J; Grant S G; Stephenson D A; Chapman V M
- CS Roswell Park Memorial Institute, Molecular and Cellular Biology Department, Buffalo, New York 14263.
- NC GM33160 (NIGMS) GM24125 (NIGMS)
- SO GENOMICS, (1988 Oct) 3 (3) 187-94. Journal code: GEN. ISSN: 0888-7543.
- CY United States
- DT Journal; Article; (JOURNAL ARTICLE)
- LA English
- FS Priority Journals
- EM 198906
- L5 ANSWER 59 OF 82 MEDLINE
- AN 88152211 MEDLINE
- DN 88152211
- TI Inactivation of tissue inhibitor of metalloproteinases by neutrophil elastase and other serine proteinases.
- AU Okada Y; Watanabe S; Nakanishi I; Kishi J; Hayakawa T; Watorek W; Travis J; Nagase H
- CS Department of Pathology, School of Medicine, Kanazawa University, Japan.
- SO FEBS LETTERS, (1988 Feb 29) 229 (1) 157-60. Journal code: EUH. ISSN: 0014-5793.
- CY Netherlands
- DT Journal; Article; (JOURNAL ARTICLE)
- LA English
- FS Priority Journals; Cancer Journals
- EM 198806
- L5 ANSWER 60 OF 82 BIOSIS COPYRIGHT 1998 BIOSIS
- AN 88:368671 BIOSIS
- DN BR35:53284
- TI PROFILE OF ACID AND NEUTRAL METALLOPROTEINASES IN OSTEOARTHRITIC OA AND IN CONTROL CARTILAGES COMPARED TO SPECIFIC TISSUE INHIBITOR OF METALLOPROTEINASE TIMP.
- AU DEAN D; PELLETIER J-P; MARTEL-PELLETIER J; HOWELL D S; WOESSNER J F
- CS V.A. MED. CENT., DEP. MED., UNIV. MIAMI SCH. MED., MIAMI, FLA. 33150.
- SO 52ND ANNUAL MEETING OF THE AMERICAN RHEUMATISM ASSOCIATION, HOUSTON, TEXAS, USA, MAY 23-28, 1988. ARTHRITIS RHEUM 31 (4 SUPPL.). 1988. S33. CODEN: ARHEAW ISSN: 0004-3591

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DT Conference
LA English
     ANSWER 61 OF 82 MEDLINE
                                                           DUPLICATE 35
L5
     88058939
                MEDLINE
ΑN
     88058939
DN
     Monocyte procollagenase and tissue inhibitor of
ΤI
     metalloproteinases. Identification, characterization, and
     regulation of secretion.
ΑU
     Campbell E J; Cury J D; Lazarus C J; Welgus H G
     Department of Medicine, Jewish Hospital at Washington University
CS
     Medical Center, St. Louis, Missouri 63110.
     HL30341 (NHLBI)
     AM35805 (NIADDK)
     HL07317 (NHLBI)
     JOURNAL OF BIOLOGICAL CHEMISTRY, (1987 Nov 25) 262 (33)
SO
     Journal code: HIV. ISSN: 0021-9258.
     United States
CY
     Journal; Article; (JOURNAL ARTICLE)
DT
     English
LΑ
FS
     Priority Journals; Cancer Journals
     198803
EΜ
     ANSWER 62 OF 82 MEDLINE
L5
     87231017
               MEDLINE
AN
DN
     87231017
ΤI
     Assignment of the TIMP gene to the murine X-chromosome
     using an inter-species cross.
     Jackson I J; LeCras T D; Docherty A J
ΑU
     NUCLEIC ACIDS RESEARCH, (1987 May 26) 15 (10) 4357. Journal code: O8L. ISSN: 0305-1048.
SO
     ENGLAND: United Kingdom
CY
     Journal; Article; (JOURNAL ARTICLE)
DT
LΑ
     English
     Priority Journals; Cancer Journals
FS
EΜ
     198709
                                                           DUPLICATE 36
L5
     ANSWER 63 OF 82 MEDLINE
ΑN
     87306864
                  MEDLINE
     87306864
DN
     Bacterial antigens induce collagenase and prostaglandin E2 synthesis
TΙ
     in human gingival fibroblasts through a primary effect on
     circulating mononuclear cells.
     Heath J K; Atkinson S J; Hembry R M; Reynolds J J; Meikle M C
ΑU
     INFECTION AND IMMUNITY, (1987 Sep) 55 (9) 2148-54. 
Journal code: GO7. ISSN: 0019-9567.
CY
     United States
     Journal; Article; (JOURNAL ARTICLE)
DT
LA
     English
FS
     Priority Journals; Cancer Journals
EM
     198712
                                                           DUPLICATE 37
     ANSWER 64 OF 82 MEDLINE
L5
     88004396
                 MEDLINE
AN
DN
     88004396
     Transforming growth factor beta modulates the expression of
TI
     collagenase and metalloproteinase inhibitor.
     Edwards D R; Murphy G; Reynolds J J; Whitham S E; Docherty A J;
ΑU
     Angel P; Heath J K
     Department of Biochemistry, University of Oxford, UK..
CS
     EMBO JOURNAL, (1987 Jul) 6 (7) 1899-904.
SO
     Journal code: EMB. ISSN: 0261-4189.
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ENGLAND: United Kingdom

CY

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Journal; Article: (JOURNAL ARTICLE)
DT
LΑ
    English
    Priority Journal
FS
EM
    198801
                                                        DUPLICATE 38
L5
    ANSWER 65 OF 82 MEDLINE
    87239677
                 MEDLINE
AN
DN
    87239677
    Human alveolar macrophages secrete an inhibitor of
TI
    metalloproteinase elastase.
    Albin R J; Senior R M; Welgus H G; Connolly N L; Campbell E J
ΑU
    HL-29594 (NHLBI)
NC
    HL-30341 (NHLBI)
    HL-07317 (NHLBI)
    AMERICAN REVIEW OF RESPIRATORY DISEASE, (1987 Jun) 135 (6)
SO
    Journal code: 426. ISSN: 0003-0805.
    United States
CY
DT
    Journal; Article; (JOURNAL ARTICLE)
LA
    English
    Abridged Index Medicus Journals; Priority Journals
FS
    198709
L5
    ANSWER 66 OF 82 MEDLINE
                                                        DUPLICATE 39
    88059565
                 MEDLINE
ΑN
    88059565
DN
TI
    Regulation of the expression of tissue inhibitor of
    metalloproteinases and collagenase by retinoids and
     glucocorticoids in human fibroblasts.
     Clark S D; Kobayashi D K; Welgus H G
ΑU
    Department of Medicine, Jewish Hospital, Washington University
    Medical Center, St. Louis, Missouri 63110.
    AM 35805 (NIADDK)
NC
    TO-AM 07284 (NIADDK)
    AM 01525 (NIADDK)
    JOURNAL OF CLINICAL INVESTIGATION, (1987 Nov) 80 (5)
SO
    1280-8.
    Journal code: HS7. ISSN: 0021-9738.
    United States
CY
    Journal; Article; (JOURNAL ARTICLE)
DΤ
LΑ
    English
    Abridged Index Medicus Journals; Priority Journals; Cancer Journals
FS
EM
    198803
    ANSWER 67 OF 82 BIOSIS COPYRIGHT 1998 BIOSIS
L5
AN 88:211054 BIOSIS
DN BR34:104064
TI A VIRUS INDUCIBLE ELEMENT CONTAINED WITHIN AN INTRON OF THE MURINE
    TISSUE INHIBITOR OF METALLOPROTEINASES TIMP GENE.
AU COULOMBE B; PONTON A; WILLIAMS B R G; SKUP D
CS INST. DU CANCER DE MONTREAL, MONTREAL, QUEBEC, CANADA H2L 4M1.
   1987 INTERNATIONAL SOCIETY FOR INTERFERON RESEARCH MEETING ON THE
    INTERFERON SYSTEM, WASHINGTON, D.C., USA, NOVEMBER 2-6, 1987. J
    INTERFERON RES 7 (6). 1987. 749. CODEN: JIREDJ ISSN: 0197-8357
DT Conference
LA English
    ANSWER 68 OF 82 MEDLINE
                                                        DUPLICATE 40
L5
AN
    87218524
              MEDLINE
DN
    87218524
    Characterization and expression of a murine gene homologous to human
TI
    EPA/TIMP: a virus-induced gene in the mouse.
    Gewert D R; Coulombe B; Castelino M; Skup D; Williams B R
ΑU
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EMBO JOURNAL, (1987 Mar) 6 (3) 651-7.

SO

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Journal code: FMS. ISSN: 0261-4189. ENGLAND: Unite Ingdom
     ENGLAND: United
CY
DΤ
     Journal; Article; (JOURNAL ARTICLE)
LΑ
     English
FS
     Priority Journals
EM
    198709
                                                         DUPLICATE 41
L5
     ANSWER 69 OF 82 MEDLINE
     88076930
               MEDLINE
AN
DN
     88076930
     Degradation of type I collagen films by mouse osteoblasts is
ΤI
     stimulated by 1,25 dihydroxyvitamin D3 and inhibited by human
     recombinant TIMP (tissue inhibitor of
     metalloproteinases).
     Thomson B M; Atkinson S J; Reynolds J J; Meikle M C
UΑ
CS
     Cell Physiology, Strangeways Research Laboratory, Worts Causeway,
     Cambridge.
     BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1987 Oct
SO
     29) 148 (2) 596-602.
     Journal code: 9Y8. ISSN: 0006-291X.
     United States
CY
     Journal; Article; (JOURNAL ARTICLE)
DT
     English
LΑ
FS
     Priority Journals; Cancer Journals
EΜ
     198803
L5
     ANSWER 70 OF 82 MEDLINE
                                                         DUPLICATE 42
NA
     88105457
                MEDLINE
DN
     88105457
     Metalloproteinases in endochondral bone formation:
TI
     appearance of tissue inhibitor-resistant metalloproteinases
    Mikuni-Takagaki Y; Cheng Y S
ΑU
     Developmental Biology Laboratory of the Medical Services,
     Massachusetts General Hospital, Boston 02114.
NC
    AM-3564 (NIADDK)
     HD-19836 (NICHD)
    ARCHIVES OF BIOCHEMISTRY AND BIOPHYSICS, (1987 Dec) 259
SO
     (2) 576-88.
     Journal code: 6SK. ISSN: 0003-9861.
CY
    United States
DT
     Journal; Article; (JOURNAL ARTICLE)
LΑ
     English
     Priority Journals; Cancer Journals
FS
    198804
EM
L5
     ANSWER 71 OF 82 MEDLINE
                                                         DUPLICATE 43
     88007986
               MEDLINE
ΑN
     88007986
DN
     Tissue inhibitor of metalloproteinases (TIMP)
TI
     regulates extracellular type I collagen degradation by chondrocytes
     and endothelial cells.
ΑU
     Gavrilovic J; Hembry R M; Reynolds J J; Murphy G
     Department of Cell Physiology, Strangeways Research Laboratory,
CS
     Cambridge, England.
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    ENGLAND: United Kingdom
CY
    Journal; Article; (JOURNAL ARTICLE)
DΤ
    English
LΑ
    Priority Journals
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DUPLICATE 44

FS

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198801

ANSWER 72 OF 82 MEDLINE

88025983 MEDLINE

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88025983
DN
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ΑU
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ΕM
     198802
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     ANSWER 73 OF 82 MEDLINE
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     198803
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DN
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FS
     Priority Journals
ΕM
     198802
L5
     ANSWER 76 OF 82 MEDLINE
     86230918
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ΑN
     86230918
DN
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ΤI
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Stricklin G P; Welgus H G

ΑU

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Journal; Article; (JOURNAL ARTICLE)

Priority Journals; Cancer Journals

ENGLAND: United Kingdom

SO

CY

DT LA

FS EM English

198704

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UPLICATE 47
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L5
ΑN
     87049506
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ΤI
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SO
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CY
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DT
LΑ
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     Priority Journals
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     198703
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L5
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AN
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ΤI
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CY
     France
     Journal; Article; (JOURNAL ARTICLE)
DT
     General Review; (REVIEW)
     English
LΑ
     Priority Journals
FS
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